

XX

Qy	1340	CCTCTCCCTTTCCCTCTCTTCTGGTCTCTTACTTCTCTCTCTCCCACTCTCCACAGC	1339
Db	1274	CCTCTCCCTTTCCCTCTCTTCTGGTCTCTTATTTCTCTCTCTCCCACTCTCCACAGC	1333
Qy	1400	CTCCTCTTTAAGCGCTGAATCAGTCTGTAGGTCATGTTTAAATCTACTACTCTTCTCTGCT	1459
Db	1334	CGCTCTTTAAGCGCTGAGTCAGTCTGAGGCCATGTTTAAATCTACTACTCTTCTCTGCT	1393
Qy	1460	CTGGACTCATCCAGATGCTCTGGCTGAGCTCTCCCTCTATCTACAATAAAACCTTCC	1519
Db	1394	CTGGACTCATCCAGATGCTCTGGCTGAGCTCTCCCTCTATCTACAATAAAACCTTCC	1452
Qy	1520	CCCTAACACAGAAATGCAAAA	1539
Db	1453	CCCTAACACAGAAATGGAACA	1472
RESULT 4			
ADM46622			
ID	ADM46622 standard; DNA; 1509 BP.		
XX	AC	AC	ADM46622;
XX	AC	AC	
DT	17-JUN-2004 (first entry)		
XX	Mouse 7F4 encoding sequence.		
XX	7F4 gene; Osteopathic; Anorectic; Antidiabetic;		
KW	glycolipid metabolism disorder; osteoporosis; obesity; diabetes; ds.		
KX			
OS	Mus musculus.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	12..542	
FT		/*tag= a	
FT		/product= "7F4"	
XX			
PN	WO2004026026-A1.		
XX			
PD	01-APR-2004.		
XX			
PF	10-SEP-2003; 2003WO-JP011545.		
XX			
PR	17-SEP-2002; 2002JP-00270321.		
XX			
PA	(CHUS) CHUGAI SEIYAKU KK.		
XX			
PI	Kake T, Saito H, Makishima F;		
XX			
DR	WPI; 2004-340227/31.		
DR	P-PSDB; ADM46623.		
XX			
PT	Transgenic non-human animal with modified expression of 7F4 gene for		
PT	screening remedies for bone or glycolipid metabolism disorders.		
XX			
PS	Claim 3; SEQ ID NO 1; 44pp; Japanese.		
XX			
CC	The present invention relates to a transgenic non-human animal having the		
CC	expression of 7F4 gene artificially modified. The transgenic animals are		
CC	a disease model for bone and glycolipid metabolism disorders. Substances		
CC	identified by the screening method are agents for the prevention and		
CC	treatment of diseases including osteoporosis, obesity and diabetes. The		
CC	present sequence represents the modified mouse 7F4 encoding sequence.		
XX			
SQ	Sequence 1509 BP; 387 A; 403 C; 294 G; 425 T; 0 U; 0 Other;		
Query Match			
Best Local Similarity		76.3%;	Score 1182.4; DB 12; Length 1509;
Matches 1321; Conservative		0;	Pred. No. 1.1e-279;
		Mismatches 101;	Indels 38; Gaps 4;
Qy	81	GCTCGTCTGCTGCTGCTGAATCTGCCCTTCAGGTAAATTTGCTATGCTAGTAATT	140
Db	50	GTTCCTCTTGTGCTGCTGCTGAATCTGTTCTGCCGTAAATTTGCTATGCTGCTGAATC	109


```

PD 29-JAN-2004.
XX
XX 17-JUL-2003; 2003US-00622407.
XX
XX 09-JUL-1999; 99US-0143063P.
XX
XX 07-JUL-2000; 2000US-00612033.
XX
XX (SARI/) SARIS C.
XX
XX Saris C;
XX
XX WPI; 2004-224390/21.
XX
XX P-PSDB; ADJ45754.
XX
XX Novel tmst2-receptor polypeptide useful for diagnosing and treating
XX disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
XX infections.
XX
XX Claim 1; SEQ ID NO 9; 57pp; English.
XX
XX The invention relates to a tmst2-receptor polypeptides and the
XX polynucleotide encoding them. The sequences of the invention are useful
XX for treating diseases and conditions including acquired immunodeficiency
XX syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral
XX malaria, diabetes mellitus, disseminated intravascular coagulation,
XX haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,
XX lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ
XX rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory
XX distress syndrome (ARDS), tuberculosis and a number of viral diseases.
XX This sequence represents cDNA encoding a murine tmst2-receptor splice
XX variant polypeptide of the invention.
XX
XX SQ Sequence 702 BP; 163 A; 177 C; 160 G; 202 T; 0 U; 0 Other;
Query Match
Best Local Similarity 38.8%; Score 602; DB 12; Length 702;
Matches 657; Conservative 0; Mismatches 0; Indels 45; Gaps 1;
Qy 1 TTGCACCTCGGCCATGTTGGCTTCTTCTGACGCTTGGTCCAGTCTGAGTCGCTGTC 60
Db 1 TTGCACCTCGGCCATGTTGGCTTCTTCTGACGCTTGGTCCAGTCTGAGTCGCTGTC 60
Qy 61 CTTTGGCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 61 CTTTGGCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 121 AAATTTGCTATGCTAGAAATACACTCTCTTCAAAATGTCCTGCTGCTGCTGCTGCTGCTG 180
Db 121 AAATTTGCTATGCTAGAAATACACTCTCTTCAAAATGTCCTGCTGCTGCTGCTGCTGCTG 180
Qy 181 GACGTCTGTTGCAAGAACTGTTCTGCAAGTACACTCTCTTCAAAATGTCCTGCTGCTGCTGCTG 240
Db 181 GACGTCTGTTGCAAGAACTGTTCTGCAAGTACACTCTCTTCAAAATGTCCTGCTGCTGCTGCTG 240
Qy 241 CATACTCAAGACAACTGAGAACTGTCACCCAGACATTCACAGAAAGATTAATTC 300
Db 241 CATACTCAAGACAACTGAGAACTGTCACCCAGACATTCACAGAAAGATTAATTC 300
Qy 301 CTGATGCTGTTATCTATCTTGTCTCACTCTGTAAGATCAGGAAATGGTGGCGACTGC 360
Db 301 CTGATGCTGTTATCTATCTTGTCTCACTCTGTAAGATCAGGAAATGGTGGCGACTGC 360
Qy 361 TCAGCCACAGTGACCGGAAATGCGAGTGGCGAATCTTACTACTATGACCCAAA 420
Db 361 TCAGCCACAGTGACCGGAAATGCGAGTGGCGAATCTTACTACTATGACCCAAA 420
Qy 421 TTTCCAGATGCTGCCGCCATGACCAAGTGTCCCAAGATCCCTGTCCTCCAGAA 480
Db 421 TTTCCAGATGCTGCCGCCATGACCAAGTGTCCCAAGTGTCCCTGTCCTCCAGAA 480
Qy 481 TGCAACTCCACAGCTAATCACTGTGTGAGTTCATCTGTTCAA----- 523
Db 481 TGCAACTCCACAGCTAATCACTGTGTGAGTTCATCTGTTCAA----- 523

```

524 -----ATCCAGAAACCGGCTGTTCTTACTGTTATCA 555
 541 GCCTGGCCTATCTGAATGGTTTCACAGAGATCCAGAAACCGGCTGTTCTTACTGTTATCA 600
 556 CTTTTCAGTGTGCTAATGTCGCTGTTGTCCTCGTATCATAGAAGATAAGGCTTC 615
 601 CTTTTCAGTGTGCTAATGTCGCTGTTGTCCTCGTATCATAGAAGATAAGGCTTC 660
 616 TACAGATGTTTCTTACGCTTCTTTTATTTGCTATGAAGTAT 657
 661 TACAGATGTTTCTTACGCTTCTTTTATTTGCTATGAAGTAT 702

RESULT 8
 AAD64758
 ID AAD64758 standard; DNA; 1200 BP.
 XX
 AC AAD64758;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Mouse tmst2-receptor-human immunoglobulin Fc region chimeric DNA.
 XX
 KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
 KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;
 KW cancer; chromosome identification; gene therapy; antibacterial; virucide;
 KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
 KW cytostatic; mouse; human; immunoglobulin Fc region; chimeric; gene; ds.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 XX CDS 1..1197
 FT /tag= a
 FT /product= "Mouse tmst2 receptor-human immunoglobulin Fc
 FT region fusion protein"
 FT /note= "No stop codon"
 FT /partial
 XX
 PN US6627199-B1.
 XX
 PD 30-SEP-2003.
 XX
 PF 07-JUL-2000; 2000US-00612033.
 XX
 PR 09-JUL-1999; 99US-0143063P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 XX Saris C;
 XX
 XX WPI; 2003-874309/81.
 XX P-PSDB; ABW02717.
 XX
 DR New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,
 XX treating or ameliorating diseases associated with or resulting from
 XX abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
 XX chromosome mapping.
 XX
 PS Example 4; SEQ ID NO 13; Opp; English.
 XX
 CC The invention relates to transmembrane decoy-receptor (tmst2) proteins
 CC and their secreted splice variants, belonging to the tumour necrosis
 CC factor (TNF) receptor super gene family and polynucleotides encoding such
 CC proteins. The composition and methods are useful in diagnosing, treating
 CC or ameliorating diseases associated with or resulting from abnormal tmst2
 CC and/or abnormal expression of its putative ligand, such as sepsis,
 CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial
 CC and parasitic diseases or cancer. They may also be used for chromosome
 CC identification or mapping. The invention is useful in gene therapy. The
 CC present sequence is a chimeric DNA comprising mouse tmst2- receptor DNA

Db 421 TCGCCCATGTACCAAGTGCCCAAGGAATCCCTGCTCCAGGAATGCAATCCACA 480
Qy 493 GCTAACACTGTGTGAGTTCATCTGTTTCAATCCAGAAACCGGCTGTTCTACTGTGA 552
Db 481 GCTAACACTGTGTGAGTTCATCTGTTTCAATGTCGACATCAGATGCCACCGTGC 540
Qy 553 TCACC 557
Db 541 CCAGC 545

RESULT 10
ADD33512/c
ID ADD33512 standard; DNA; 503 BP.
AC ADD33512;
XX
DT 15-JAN-2004 (first entry)
XX
DE Mouse mitochondrial DNA sequence SEQ ID NO:1285.
XX
KW ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
KW mitochondrial disease; oxidative phosphorylation dysfunction;
KW oxidative stress; apoptosis; aging.
XX
OS Mus musculus.
XX
PN WO2003020220-A2.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-US027886.
XX
PR 30-AUG-2001; 2001US-0316323P.
XX
PR 31-AUG-2001; 2001CA-02356540.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Wallace DC, Levy S, Kerstann K, Procaccio V;
XX
DR WPT; 2003-300821/29.
XX
XX Array containing probes for genes involved in mitochondrial biology,
XX useful for determining mitochondrial biology gene expression profiles for
XX use in diagnosing pathologies and identifying biochemical pathways.
XX
XX Claim 2; SEQ ID NO 1285; 201pp; English.

XX The invention relates to a novel array comprising at least two isolated
XX nucleotide molecules, each molecule having a sequence capable of uniquely
XX hybridising to a nucleic acid molecule which is an expression product of
XX a gene involved in mitochondrial biology. The array comprises two or more
XX isolated nucleic acid molecules or spots, each molecule having a sequence
XX chosen from sequence of 994 human probes and 2046 mouse probes. An array
XX of the invention is useful for determining an expression profile of a
XX mouse or human sample containing nucleic acid, by contacting the array
XX with the sample under conditions allowing selective hybridisation, and
XX measuring hybridisation of nucleic acid in the sample to the array to
XX produce an expression profile. The array is also useful for determining
XX an expression profile of a first labelled sample containing nucleic acid
XX relative to a second, differently labelled sample containing nucleic
XX acid. The second sample is a reference or a standard. An array is useful
XX for determining an expression profile diagnostic of an energy-metabolism-
XX related physiological condition. An array of the invention is useful for
XX determining mitochondrial biology gene expression profiles of organisms,
XX such as human, mice and closely related species, tissue and organs of
XX such organisms, which are useful for determining expression profiles
XX diagnostic of energy metabolism-related physiological conditions,
XX diagnosing such physiological conditions, identifying biochemical
XX pathways, genes, and mutations involved in such physiological conditions,
XX identifying therapeutic agents useful for preventing and/or treating such
XX physiological conditions, evaluating and/or monitoring the efficacy of

CC such therapies, and creating and identifying animal models of human
CC energy metabolism-related physiological conditions. An array is also
CC useful for defining expression signatures or profiles for mitochondrial
CC diseases, as well as distinguishing clinical disorders that result from
CC oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,
CC apoptosis and aging. An array of the invention contains probes of genes
CC not previously recognised to participate in mitochondrial biology. The
CC sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA
CC clones used to make the probes of the invention. Some sequences are not
CC present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
CC 1906, 2408 and 2643.
XX

Qy 1025 ATTTCTTATGAGGCAAGCATTCAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACC 1084
Db 503 ATTTCTTATGAGGCAAGCATTCAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACC 444
Qy 1085 ACCACAGGTTAAACAATTCCTCTGAGGCTCTCTGTTGAGGGCCCTCTTGGAGTAAAGT 1144
Db 443 ACCACAGGTTAAACAATTCCTCTGAGGCTCTCTGTTGAGGGCCCTCTTGGAGTAAAGT 384
Qy 1145 AACAAATTTAGATGAAGGCAAGTCTCTGATCAGGTCCAAAGAAACTCAGGATGAATGGT 1204
Db 383 AACAAATTTAGATGAAGGCAAGTCTCTGATCAGGTCCAAAGAAACTCAGGATGAATGGT 324
Qy 1205 CCAGTGTGGTTCCTATTAAACATGAGTGAAGAAACATGACCTCAGCTTACAGCTCCACCTC 1264
Db 323 CCCTGTGGTTCCTATTAAACATGAGTGAAGAAACATGACCTCAGCTTACAGCTCCACCTC 264
Qy 1265 ACTGACTTCCCTCCCTAGCTTCTCATTCAGAGTAACCTGCATTTTGGTAATGT 1324
Db 263 ACTGGCTTCCCTCCCTAGCTTCTCATTCAGAGTAACCTGCATTTTGGTAATGT 204
Qy 1325 GCCTTCTTGGTTCCTCTCTCTTCCCTCTCTTCTGTTGCTTCTTCTTCTCTCTCTCTC 1384
Db 203 GCCTTCTTGGTTCCTCTCTCTTCCCTCTCTTCTGTTGCTTCTTCTTCTCTCTCTC 144
Qy 1385 CCAGTCTCCAGAGCTCTCTTAAAGGCTGAATCAGTCTGAGTCAATGTTAATCTAC 1444
Db 143 CCAGTCTCCAGAGCTCTCTTAAAGGCTGAATCAGTCTGAGTCAATGTTAATCTAC 86
Qy 1445 TACTTTCTCTCTCTCTGAGTCTCATCCAGATGCTCTGAGTCTCTCTCTCTCTCTCTA 1504
Db 85 TACTTTCTCTCTCTCTGAGTCTCATCCAGATGCTCTGAGTCTCTCTCTCTCTCTA 26
Qy 1505 CAATAAAACCTTCCCTTAACCCAG 1529
Db 25 CAATAAAACCTTCCCTTAACCCAG 1

RESULT 11
ADD33513
ID ADD33513 standard; DNA; 603 BP.
XX
AC ADD33513;
XX
DT 15-JAN-2004 (first entry)
XX
DE Mouse mitochondrial DNA sequence SEQ ID NO:1286.
XX
KW ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
KW mitochondrial disease; oxidative phosphorylation dysfunction;
KW oxidative stress; apoptosis; aging.
XX
OS Mus musculus.
XX
PN WO2003020220-A2.
XX

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C	1	1550	100.0	1550	6	AR403753 Sequence
	2	1537.6	99.2	1555	10	AY046551 Mus muscu
	3	1207	77.9	1491	10	AY155625 Mus muscu
	4	1182.4	76.3	1509	6	AR164284 Sequence
	5	1016	65.5	203141	10	AC068006 Mus muscu
	6	1016	65.5	281000	10	MMU275605 Mus muscu
	7	673	43.4	691	10	AY165627 Mus muscu
	8	618	39.9	736	10	AY165626 Mus muscu
	9	602	38.8	702	6	AR403754 Sequence
C	10	514.6	33.2	1200	6	AR403757 Sequence
	11	494.6	31.9	669	10	MMU278265 Mus muscu
	12	435.8	28.1	240262	2	AC129151 Rattus no
	13	412	26.6	412	6	AR403752 Sequence
	14	407.8	26.3	569	10	MMU278264 Mus muscu
	15	402.2	25.9	531	10	AY046550 Mus muscu
	16	232	15.0	217774	2	AC120603 Rattus no
	17	232	15.0	232893	2	AC096182 Rattus no
	18	232	15.0	286646	2	AC127881 Rattus no
C	19	231.4	14.9	131919	10	AC096622 Mus muscu

Db	241	CAAGGACAATGTGAGAAAGTGTCAACCGAGAACATTTACAGAGAAAGATATTTACCTGGAT	300
Qy	307	GCCTTGTATATCTTTGCTCCACCTGTGATAAAGATCAGAAATGGTGGCCGACTGCTCAGCC	366
Db	301	GCCTTGTATATCTTTGCTCCACCTGTGATAAAGATCAGAAATGGTGGCCGACTGCTCAGCC	360
Qy	367	ACCAGTGACCGGAAAATGCCAGTGCAGATCCGNAACAGGTCTTTACTACTATGACCCAAAATTTCCA	426
Db	361	ACCAGTGACCGGAAAATGCCAGTGCAGATCCGNAACAGGTCTTTACTACTATGACCCAAAATTTCCA	420
Qy	427	GAATCGTGCGCCCATGTATCAACAGTGTCCCAAGGAATCCCTGCTCTCCAGGAATGCAAC	486
Db	421	GAATCGTGCGCCCATGTATCAACAGTGTCCCAAGGAATCCCTGCTCTCCAGGAATGCAAC	480
Qy	487	TCCACAGCTAAACACTGTGTGCAGTTCACTGTGTTTTCAAATCCAGAAAACCGGCTGTTCTTA	546
Db	481	TCCACAGCTAAACACTGTGTGCAGTTCACTGTGTTTTCAAATCCAGAAAACCGGCTGTTCTTA	540
Qy	547	CTGTTATCACTTTGAGTGTGCTAAATGTGTGTCGTTGTGTCTTCGTATCATAGAAGA	606
Db	541	CTGTTATCACTTTGAGTGTGCTAAATGTGTGTCGTTGTGTCTTCGTATCATAGAAGA	600
Qy	607	TAAAGTTCTACAGATGTTTTCTTAGCTTCCTTTATTGCTATGAAGTGAATCATATGGAG	666
Db	601	TAAAGTTCTACAGATGTTTTCTTAGCTTCCTTTATTGCTATGAAGTGAATCATATGGAG	660
Qy	667	GCAACTCTTTATTTATTTATTTATTTATTTATTTTAAATGTCTGAACTTGATTTGAAG	726
Db	661	GCAACTCTTTATTTATTTATTTATTTATTTTAAATGTCTGAACTTGATTTGAAG	720
Qy	727	ACCAAGGTGCGCTCAAAATCACAGAGATCCAGACTAAGACAACCTCTAATTAAGGGAACAT	786
Db	721	ACCAAGGTGCGCTCAAAATCACAGAGATCCAGACTAAGACAACCTCTAATTAAGGGAACAT	780
Qy	787	TTAATTTGGGACTGCTTTACAGTTTCGACGTTTTGTCCATGATTTATCATAGTGGGAAGCA	846
Db	781	TTAATTTGGGACTGCTTTACAGTTTCGACGTTTTGTCCATGATTTATCATAGTGGGAAGCA	840
Qy	847	TGGCAGCATCTTAAGCAGACATGATGTTTGGAGAAAGAGCTGAGATTTCTGCATCTTGATCT	906
Db	841	TGGCAGCATCTTAAGCAGACATGATGTTTGGAGAAAGAGCTGAGATTTCTGCATCTTGATCT	900
Qy	907	GCAAGCAATAAAGGAGACTGTGTGCCACACTATACACAGCTTGAAACATTAAGGAGACCTCA	966
Db	901	GCAAGCAATAAAGGAGACTGTGTGCCACACTATACACAGCTTGAAACATTAAGGAGACCTCA	960
Qy	967	AAGCCTGTCCCCACAGTGAACAACTTCTCCAAACAGGTCTACCTCCTTAATATACCAT	1026
Db	961	AAGCCTGTCCCCACAGTGAACAACTTCTCCAAACAGGTCTACCTCCTTAATATACCAT	1020
Qy	1027	TTCTTATGAGGCAAGCATTTCAACACATGAGTCTATGAGGCCCCAAACCAATTCAAACCCAC	1086
Db	1021	TTCTTATGAGGCAAGCATTTCAACACATGAGTCTATGAGGCCCCAAACCAATTCAAACCCAC	1080
Qy	1087	CACAGGTTAAACAATGGCCCTCTGCAGCTCTCTGTGTGAGGCCCTCTCTTGAGAGTAAGTAA	1146
Db	1081	CACAGGTTAAACAATGGCCCTCTGCAGCTCTCTGTGTGAGGCCCTCTCTTGAGAGTAAGTAA	1140
Qy	1147	CAATTTAGATGAAGCAAGTCTCGGTATCAGGTCCTAAAGAACTCAGGATGATGTGTC	1206
Db	1141	CAATTTAGATGAAGCAAGTCTCGGTATCAGGTCCTAAAGAACTCAGGATGATGTGTC	1200
Qy	1207	ACTGTGGTTCCTATTAAACATACTGAAGAAACATGACCTCACCTTACAGCTCTCCACCTCAC	1266
Db	1201	ACTGTGGTTCCTATTAAACATACTGAAGAAACATGACCTCACCTTACAGCTCTCCACCTCAC	1260
Qy	1267	TGACTTCCCTTCCCCTAGCTTCTCATATCCCAAGGTAACCTGCCAATTTTTTGGTAAATGTGC	1326
Db	1261	TGACTTCCCTTCCCCTAGCTTCTCATATCCCAAGGTAACCTGCCAATTTTTTGGTAAATGTGC	1320
Qy	1327	CTTCTTGGTTCCTTCTCTCTTCCCTCTCTTCTGGTCTTTACTTCTCTTCTCTCTCCC	1386
Db	1321	CTTCTTGGTTCCTTCTCTCTTCCCTCTCTTCTGGTCTTTACTTCTTCTTCTCTCTCCC	1380

QY	1387	ACTCTCCACGAGCTCTCTTTAAGGCTGAATCAGTCTGTAGTCACTGTTTAACTACTA	1444
DB	1381	ACTCTCCACGAGCTCTCTTTAAGGCTGAATCAGTCTGTAGTCACTGTTTAACTACTA	1440
QY	1447	CTTTCTCTCTGCTCTGAGTCATCCAGATCTCTCGCTGAGCTCTCCCTCTCTATCTACA	1506
DB	1441	CTTTCTCTCTGCTCTGAGTCATCCAGATCTCTCGCTGAGCTCTCCCTCTCTATCTACA	1500
QY	1507	ATAAAACCTTTCCCTTAACAGAAATGCAAAAAA	1550
DB	1501	ATAAAACCTTTCCCTTAACAGAAATGCAAAAAA	1544
RESULT 3	AY165625	1491 bp	linear
LOCUS	Mus musculus decoy TRAIL receptor 1 (Dctrailr1)	1491 bp	linear
DEFINITION	Mus musculus decoy TRAIL receptor 1 (Dctrailr1)	1491 bp	linear
ACCESSION	AY165625	GI:27985587	1491 bp
VERSION	AY165625.1	GI:27985587	1491 bp
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 1491)		
AUTHORS	Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovskoy, A., Gong, D., Dobles, M., Hertig, S., Hofmann, K., Van Vlijmen, H., Hsu, Y.-M., Burkly, L., Tschopp, J. and Zheng, T.S.		
TITLE	Identification of a New Murine Tumor Necrosis Factor Receptor Locus That Contains Two Novel Murine Receptors for Tumor Necrosis Factor-related Apoptosis-inducing Ligand (TRAIL)		
JOURNAL	J. Biol. Chem. 278 (7), 5444-5454 (2003)		
PUBMED	12466268		
REFERENCE	22 (bases 1 to 1491)		
AUTHORS	Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovskoy, A., Gong, D., Dobles, M., Hertig, S., Hofmann, K., Van Vlijmen, H., Hsu, Y.-M., Burkly, L., Tschopp, J. and Zheng, T.S.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-OCT-2002) Institute of Biochemistry, University of Lausanne, Boveresses 155, Epalinges CH-1066, Switzerland		
FEATURES	Location/Qualifiers		
source	1..1491		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/strain="C57BL"		
	/db_xref="taxon:10090"		
	/chromosome="7"		
gene	1..1491		
	/gene="Dctrailr1"		
	/note="synonym: Tnfrh1"		
CDS	7..537		
	/product="decoy TRAIL receptor 1"		
	/protein_id="AA087805.1"		
	/db_xref="GI:27985588"		
	/translation="MWTFSHVSSLSHWFLLLLLNLPVIFAMPESYSFNCPDGVEYQVSNVCCCKTSGTGVPAKPIPTGQCEKHPGTFTKGKGLHDCSLCTCDKQDQNNVADCSATSDRKECQIGLYYYDPKFPESCRPTCKPQIGIPVLQCNSTANTVTCSSSVSVNPRWFLMLLIIVCI"		
ORIGIN			
Query Match	77.9%	Score 1207;	DB 10; Length 1491;
Best Local Similarity	90.7%	Pred. No. 4.6e-285;	
Matches 1334; Conservative	0;	Mismatches 100;	Indels 37; Gaps 3;
QY	81	GCTGTCGTCTGCTGCTGCTGAATCTGCCCTTCAGAGTAAATTTGCTATGCTAGATT	140
DB	45	GTTCCTCTTGTCTGCTGCTGAATCTGCTTTCGCGGTAAATTTGCTATGCTGCTGAAT	104

Qy	441	ATGTACCAAGTGTCCCAAGAAATCCCTGTCTCTCCAGGAATGCAATCTCCACAGCTAACAC	500
Db	410	ATGTACCAAGTGTCCCAAGAAATCCCTGTCTCTCCAGGAATGCAATCTCCACAGCTAACAC	469
Qy	501	TGTGTGAGTTCATCTGTTCCTCAAAATCCAGAAACCGGCTGTCTCTACTGTATTATCACCTTT	560
Db	470	TGTGTGAGTTCATCTGTTCCTCAAAATCCAGAAATCGGCTGTTCCTACTGAT-----	520
Qy	561	GAGTGTGCTAATTGTGTCCGTTGTGTCTTCCGTTATCATTAAGAGATATAAAGTTCTACAG	620
Db	521	-----GCTAATTGTCTCTGTATCTGAAGAAGATAAAGTTCTACAG	562
Qy	621	ATGTTTCTT-TAGCTTCCTTTATTTGCTATGAAGTGATATATGGAGGCAACTCTTTTAT	679
Db	563	ATGGTGTCTGTAGCTTCCTTTATTTGCTGTGAAGAGAAACCATGGAGGCAACTCT-----	617
Qy	680	TTTATTTATTTTATTTTATTTTAAATGCTTTGAACTTTGATTTTGAAGACCAAGCTGGCCT	739
Db	618	-----TTCATTTTATTTTATTTTAAATGCTTTGAACTTTGATTTTGAAGACCAAGCTGGACT	673
Qy	740	CAAAATCACAGAGATCCAGACTAAGACAACCTCTAATAAGGGAAACATTTAATTGGGACTG	799
Db	674	CAAACTCACAGAGATCCGACTAGGCACCTCTAATATAGGAAACATTTGAATTGGGACTG	733
Qy	800	GCTTACAGTTTCGACGCTTTTGTCCATGATTATCATAGTGGGAGCAATGCGAGCATCTAA	859
Db	734	GCTTACAGTTTCAGAAGTTCTGTCCATGATTATCATAGTGCAGGATGATGAGGCGACGGAG	793
Qy	860	GCAGACATGATGTTGGAGAGGAGCTGAGATTTCTGCATCTTGATCTGCAAGCAATAAAA	919
Db	794	GCACACATGTTGCTGGAGAGAGAGCTGAGAGTTCTGCACTCTGATCTGCAAGCAATAAAA	853
Qy	920	GGAGACTGTGTGCCACACTATACACAGCTTGGAAATAGGAGACCTCAAAAGCCTGTCCCA	979
Db	854	GGAGACTGTGTGCCACACTACACATAGCTTGGACATAGGAGACCTCAAAAGCCTGTCCCA	913
Qy	980	CAGTGAACAATCTCTCTCCAAAGGTCATACCTCTTAATAATACCATTTCTTAGAGGCA	1039
Db	914	CAGTGAACAATCTCTCTCCAAAGGTCATACCTCTTAATAATACCATTTCTTAGAGGCA	973
Qy	1040	AGCAATCAAAACATAGTCTTAGAGGGCCAAACCAATTCAAACCCACACAGGTTAACAA	1099
Db	974	AGCAATCAAAACATAGTCTTAGAGGGCCAAACCAATTCAAACCCACACAGGTTAACAA	1033
Qy	1100	TTGGCCTCTGCAGCTCTCTGGTGGAGGCCCTCTTGAGAGTAAAGTAAACAATTTAGATGAA	1159
Db	1034	TTGGCCTCTGCAGCTCTCTGGTGGAGGCCCTCTTGAGAGTAAAGTAAACAATTTAGATGAA	1093
Qy	1160	GGCAAGTCTGGTATCAGGTCCTCAAAAGAAATCTAGGATGAATGGTCCATGTGGTTCTTA	1219
Db	1094	GGCAAGTCTGGTATCAGGTCCTCAAAAGAAATCTAGGATGAATGGTCCATGTGGTTCTTA	1153
Qy	1220	TTAACATCTAGGAAGAACATGACCTCACCTTTACAGCTCTCAACCTCACTGATTCCTTCC	1279
Db	1154	TTAACATCTAGGAAGAACATGACCTCACCTTTAGACTTCTCCACCTCACTGGCTTCCCTTCC	1213
Qy	1280	CCTAGCTTCTCATTTCCAGGTAAACCTGCCATTTTGGTAAATGTGCTTCTTGGTTCTTT	1339
Db	1214	CCTAGCTTCTCATTTCCAGGTAAACCTGCCATTTTGGTAAATGTGCTTCTTGGTTCTTT	1273
Qy	1340	CCTCTCCTTTTCCCCCTCTCTTTCTGGTCCCTTACTTCTCTCTCCCTCCCACTCTCCACGAGC	1399
Db	1274	CCTCTCCTTTTCCCCCTCTCTTTCTGTGCTCTTATTTCTCTCTCTCCCACTCTCCACGAGC	1333
Qy	1400	CTCCTCTTAAGGCCCTGAATCAGTCTGTAGGTCATGTTTAAATCTACTACTTTCTCTGTCT	1459
Db	1334	CGCCTCTTAAGGCCCTGAGTCAGTCTGAGGCCATGTTTAAATCTACTACTTTCTCTGTCT	1393
Qy	1460	CTGAGCTCATCCAGATGTCTGTGCTGAGCTCTCCCTCTTATCTACAAATAAAACCTTCC	1519
Db	1394	CTGAGCTCATCCAGATGTCTGTGCTGAGCTCTCCCTCTTATCTACAAATAAA-CTTCC	1452
Qy	1520	CCCTAAACCAAGAAATGCAAAA	1539

QY	792	TGGGACTGCGTTACAGTTTTCGGACGTTTTGTCCATGATATCATAGTGGGAAGCATGGCA	851
Db	78947	TGGGACTGCGTTACAGTTTTCGGACGTTTTGTCCATGATATCATAGTGGGAAGCATGGCA	79006
QY	852	GCATCTAAGCAGACATGATGTTTGGAGAGGAGCTCAGATTTTCGCATCTTCATCTGCAAG	911
Db	79007	GCATCTAAGCAGACATGATGTTTGGAGAGGAGCTCAGATTTTCGCATCTTCATCTGCAAG	79066
QY	912	CAATAAAGGAGACTGTGTGSCACACTATACACAGCTTTGAACATAGGAGACCTCAAGGCC	971
Db	79067	CAATAAAGGAGACTGTGTGSCACACTATACACAGCTTTGAACATAGGAGACCTCAAGGCC	79126
QY	972	TGTTCCCAACAGTGACAAACTTCTCCACACAGGTCATACCTCTCTAATAAATACCAATTTCTT	1031
Db	79127	TGTTCCCAACAGTGACAAACTTCTCCACACAGGTCATACCTCTCTAATAAATACCAATTTCTT	79186
QY	1032	ATGAGGCAAGCAATTCAAAACACATGAGTCTATCAGAGGGCCAAACCAATTCAAAACCAACACAG	1091
Db	79187	ATGAGGCAAGCAATTCAAAACACATGAGTCTATCAGAGGGCCAAACCAATTCAAAACCAACACAG	79246
QY	1092	GTTTAACAATTTGCCCTCTGCAGCTCTCTGTGTGAGGCCCTCTCTTGAGAGTAAGTAACAAATT	1151
Db	79247	GTTTAACAATTTGCCCTCTGCAGCTCTCTGTGTGAGGCCCTCTCTTGAGAGTAAGTAACAAATT	79306
QY	1152	TAGATGAAGGCAAGTCTCGGTATCAGGTCACAAAGAACTCAGGATGAATGGTCCACTGT	1211
Db	79307	TAGATGAAGGCAAGTCTCGGTATCAGGTCACAAAGAACTCAGGATGAATGGTCCACTGT	79366
QY	1212	GGTTCTATTACATACCTGAAGAACATGACCTCAGCTTACACGCTCCACCTCACTGACT	1271
Db	79367	GGTTCTATTACATACCTGAAGAACATGACCTCAGCTTACACGCTCCACCTCACTGACT	79426
QY	1272	TCCTTTCCCTAGCTTCTCATTTCCAGGTAACCCCTGCCAATTTTTGGTAATGTGCTTCT	1331
Db	79427	TCCTTTCCCTAGCTTCTCATTTCCAGGTAACCCCTGCCAATTTTTGGTAATGTGCTTCT	79486
QY	1332	TGTTCTCTCTCTCTCTTTCCCTCTCTTCTGGCTCTTAATCTCTCTCTCTCTCTCTCTCT	1391
Db	79487	TGTTCTCTCTCTCTCTTTCCCTCTCTTCTGGCTCTTAATCTCTCTCTCTCTCTCTCTCT	79546
QY	1392	CCACGAGCTCTCTTTAAGGCTGATCAGTCTGTAGTGCATGTTTAACTTACTACTCTTC	1451
Db	79547	CCACGAGCTCTCTTTAAGGCTGATCAGTCTGTAGTGCATGTTTAACTTACTACTCTTC	79606
QY	1452	TCCTCTCTCTGGAAGTCTCATCCAGATGTCCTCGGCTGAGTCTCCCTCTCTCTCAATAAA	1511
Db	79607	TCCTCTCTCTGGAAGTCTCATCCAGATGTCCTCGGCTGAGTCTCCCTCTCTCTCAATAAA	79666
QY	1512	ACCTTTCCCTCAACAGAAATGCAAAA	1539
Db	79667	ACCTTTCCCTCAACAGAAATGCAACA	79694
RESULT 7			
AY165627			
LOCUS			
DEFINITION	AY165627 691 bp mRNA linear ROD 19-FEB-2003		
ACCESSION	Mus musculus decoy TRAIL receptor 2 long form (Dctrailr2) mRNA,		
VERSION	complete cds; alternatively spliced.		
KEYWORDS	AY165627		
SOURCE	AY165627.1 GI:27986023		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Mus musculus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
JOURNAL	1 (bases 1 to 691)		
	Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovskoy, A.,		
	Gong, D., Dobles, M., Herzig, S., Hofmann, K., Van Vlijmen, H.,		
	Hau, Y.-M., Burkle, L., Tschopp, J. and Zheng, T. S.		
	Identification of a New Murine Tumor Necrosis Factor Receptor Locus		
	That Contains Two Novel Murine Receptors for Tumor Necrosis		
	Factor-related Apoptosis-inducing Ligand (TRAIL)		
	J. Biol. Chem. 278 (7), 5444-5454 (2003)		


```
Db 501 |-----GCTAATGCTCTCTGTAATCTGAAGAGATAAAGGTTCTACAG 542
Qy 621 ATGTTTCT-TAGCTTCTCTTTTATTC 646
Db 543 ATGTTCTCTAGTCTCTTTTATTC 569

RESULT 15
AY046550
LOCUS Mus musculus TNF receptor family member SOB mRNA, complete cds.
DEFINITION Mus musculus TNF receptor family member SOB mRNA, complete cds.
ACCESSION AY046550
VERSION AY046550.1 GI:18056433
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 531)
AUTHORS Pan, G., Mao, W. and Risser, P.
TITLE Characterization of SOB, a member of the TNFR family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 531)
AUTHORS Pan, G.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2001) Molecular Oncology, Genentech, Inc. 1 DNA
Way, South San Francisco, CA 94080, USA
FEATURES
source 1..531
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
CDS 1..531
/codon_start=1
/product="TNF receptor family member SOB"
/protein_id="AAL05072.1"
/db_xref="GI:18056434"
/translations="MVFSHVSLSHWFLLLNLNLFVIFAMPESYSFNCPDGEYQ
SNDVCKTCSGTFVAPCKIPHTQCKCHPGTFTGKONGLHDCLELSTCDKQDM
VADCSATSRKCSQIGLYYDPPKPPESCRPCTKCPQIPVLQECNSTANTVCSSVS
NPNWFLMLLIVFCI"

ORIGIN
Query Match 25.9%; Score 402.2; DB 10; Length 531;
Best Local Similarity 90.9%; Pred. No. 1e-87;
Matches 428; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Qy 81 GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGACAGTAAATTTGCTATGCTAGAAAT 140
Db 39 GTTCCTCTTCTGCTGCTGCTGAATCTGTTCTGCCGTAATATTTGCTATGCTGAATC 98
Qy 141 ACACTCCTCAATGTCCTGCTGCTGAATCTGCTCTAAGAGAGCTGTTTGCAAGAACTG 200
Db 99 ATACTCCTTCAACTGTCCTGCTGCTGAATCTGCTCTAAGAGAGCTGTTTGCAAGAACTG 158
Qy 201 TTCTGACAGTACATTTTCTCAAGCGCCCTCGAAATCCCTCATCTCAAGGACAATGTGA 260
Db 159 TCCTCAGGTACATTTTCTCAAGCGCCCTCGAAATCCCTCATCTCAAGGACAATGTGA 218
Qy 261 GAAGTGTCAACCCAGGAACATTTCAAGAGAAAGATAATTAATCTGGATGCTTTGTATCTTTG 320
Db 219 GAAGTGTCAACCCAGGAACATTTCAAGGAAAGATAATGCGCTGCTGATTTGTGAATTTG 278
Qy 321 CTCCACCTGTATTAAGATCAGGAATGTTGGCGACTGCTCAGCCACAGTACCCGGAA 380
Db 279 CTCCACCTGTATTAAGATCAGGAATGTTGGCGACTGCTGCTCAGCCACAGTACCCGGAA 338
Qy 381 ATGCCAGTCCGACAGCTCTTTACTACTATGACCCCAAAATTTCCAGAAATCGTGCCGCC 440
Db 339 ATGCCAGTCCGACAGCTCTTTACTACTATGACCCCAAAATTTCCGAAATCATGCCGCC 398
Qy 441 ATGTACCAAGTGTCCCAAGGAATCCCTGCTCTCCAGGAATGCAACTCCACAGCTAACAC 500
```

```
Db 399 ATGTACCAAGTGTCCCAAGGAATCCCTGCTCTCCAGGAATGCAACTCCACAGCTAACAC 458
Qy 501 TGTGTGCAAGTTCATCTCTGTTTCAAAATCCAGAAACCGGCTGTTCTCTACTGTT 551
Db 459 TGTGTGCAAGTTCATCTCTGTTTCAAAATCCAGAAACCGGCTGTTCTCTACTGAT 509
```

Search completed: September 8, 2005, 23:31:23
Job time : 15939.5 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 15:59:37 ; Search time 779.13 Seconds
(without alignments)
3255.208 Million cell updates/sec

Title: US-10-622-407-7
Perfect score: 1550
Sequence: 1 ttgcactcgccatgtttgg.....aatgcaaaaaaaaaaaaaa 1550

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1550	100.0	1550	4	US-09-612-033B-7
2	1182.4	76.3	1509	3	US-09-411-722-3
3	1182.4	76.3	1509	4	US-09-855-266A-3
4	602	38.8	702	4	US-09-612-033B-9
5	514.6	33.2	1200	4	US-09-612-033B-13
6	412	26.6	412	4	US-09-612-033B-5
7	96.6	6.2	3791	3	US-08-675-773B-3
8	88.4	5.7	51259	3	US-08-781-891-209
9	88.4	5.7	51259	4	US-09-618-166-209
10	85.2	5.5	7218	1	US-08-232-463-14
11	81.4	5.3	30310	4	US-09-657-346A-96
12	78.5	5.1	3872	5	PCT-US93-12169-1
13	74.2	4.8	4243	3	US-08-477-831C-7
14	74.2	4.8	5257	4	US-09-917-254-47
15	74	4.8	90050	3	US-09-245-041-5
16	74	4.8	90050	4	US-09-358-055B-5
17	74	4.8	90050	4	US-09-893-238-5
18	55.2	3.6	872	4	US-09-509-712B-48
19	54	3.5	1225	4	US-09-569-098A-99
20	52.4	3.4	3611	2	US-08-727-118-1
21	50.6	3.3	113042	4	US-09-949-016-12343
22	50.6	3.3	113042	4	US-09-949-016-15246
23	48.8	3.1	325	2	US-08-531-927B-3
24	47.6	3.1	1776	2	US-08-531-927B-1
25	47.6	3.1	1776	3	US-09-041-886-12
26	47.6	3.1	2224	4	US-09-922-364A-44
27	47.6	3.1	2224	4	US-09-254-590-44

C 28	47.6	3.1	2224	4	US-10-115-415-44	Sequence 44, Appl
C 29	47.6	3.1	2224	4	US-10-116-260-44	Sequence 44, Appl
C 30	47.6	3.1	2224	4	US-10-115-671-44	Sequence 48, Appl
C 31	47.6	3.1	2462	4	US-09-922-364A-48	Sequence 48, Appl
C 32	47.6	3.1	2462	4	US-09-254-590-48	Sequence 48, Appl
C 33	47.6	3.1	2462	4	US-10-115-415-48	Sequence 48, Appl
C 34	47.6	3.1	2462	4	US-10-116-260-48	Sequence 48, Appl
C 35	47.6	3.1	2462	4	US-10-115-671-48	Sequence 48, Appl
C 36	47.4	3.1	321022	4	US-09-949-016-11852	Sequence 11852, A
C 37	47.4	3.1	321022	4	US-09-949-016-14166	Sequence 14166, A
C 38	47.2	3.0	601	4	US-09-253-691-3	Sequence 3, Appl
C 39	47.2	3.0	601	4	US-09-949-016-44973	Sequence 44973, A
C 40	47.2	3.0	601	4	US-09-949-016-44974	Sequence 44974, A
C 41	47.2	3.0	2514	4	US-09-949-016-1290	Sequence 1290, Ap
C 42	47.2	3.0	165651	4	US-09-949-016-13032	Sequence 13032, A
C 43	46	3.0	3302	4	US-09-620-312D-475	Sequence 475, App
C 44	46	3.0	90050	3	US-09-245-041-5	Sequence 5, Appl
C 45	46	3.0	90050	4	US-09-358-055B-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-612-033B-7
; Sequence 7, Application US/09612033B

; Patent No. 6627199

; GENERAL INFORMATION:

; APPLICANT: Saris, Chris

; TITLE OF INVENTION: Isolation, Identification, and Characterization of

; TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily

; FILE OF INVENTION: of Genes

; FILE REFERENCE: 01017/35434A

; CURRENT APPLICATION NUMBER: US/09/612,033B

; CURRENT FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,063

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1550

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (13)..(606)

; OTHER INFORMATION: mouse tmst2

US-09-612-033B-7

Query Match 100.0%; Score 1550; DB 4; Length 1550;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTGCAC	TGGCCCAATGTTGGCTTCTTTCG	CAGTGGTCCAGTCTGAGTCGCTGTC	60
Db	1	TTGCAC	TGGCCCAATGTTGGCTTCTTTCG	CAGTGGTCCAGTCTGAGTCGCTGTC	60
Qy	61	CTTTGG	CGGCGGTGCTGCTGCTGCTGCTG	CTGCTGCTGAATCTGCCCTTGCAGGTA	120
Db	61	CTTTGG	CGGCGGTGCTGCTGCTGCTGCTG	CTGCTGCTGAATCTGCCCTTGCAGGTA	120
Qy	121	AAATTT	GTCTATGTAGAATTTACACTCCTT	CAAAATGTCCTGCTGGTGAATACTGGTCTAAA	180
Db	121	AAATTT	GTCTATGTAGAATTTACACTCCTT	CAAAATGTCCTGCTGGTGAATACTGGTCTAAA	180
Qy	181	GAGCTC	TGTTGCAAGAACTGTTCTG	CAGGTACATTTGTCAAGGCGCCCTCGGAATCCCC	240
Db	181	GAGCTC	TGTTGCAAGAACTGTTCTG	CAGGTACATTTGTCAAGGCGCCCTCGGAATCCCC	240
Qy	241	CATAC	TCAAGGACAATGTGAGAGTGT	CACCCAGGAACTTTCACAGAGAAGATAATTAC	300
Db	241	CATAC	TCAAGGACAATGTGAGAGTGT	CACCCAGGAACTTTCACAGAGAAGATAATTAC	300

```
Qy 301 CTGGATCGTTGTATACCTTGGCTCACCTGTGATATAAGATCAGGAATGGTGGCGACTGC 360
Db 301 CTGGATCGTTGTATACCTTGGCTCACCTGTGATATAAGATCAGGAATGGTGGCGACTGC 360
Qy 361 TCAGCCACCAAGTACCGGAATGCGAGTGGCGGAACAGTCTTTACTACTATGATGACCCAAAA 420
Db 361 TCAGCCACCAAGTACCGGAATGCGAGTGGCGGAACAGTCTTTACTACTATGATGACCCAAAA 420
Qy 421 TTTCCAGAAATCGTCCGCCCATGTACCAAGTGTCCCAAGGAATPCCCTGTCTCCAGGAA 480
Db 421 TTTCCAGAAATCGTCCGCCCATGTACCAAGTGTCCCAAGGAATPCCCTGTCTCCAGGAA 480
Qy 481 TGCAACTCCACAGCTAACACTGTGTGCGAGTTCATCTGTTTCAAAATCCAGAAACCGGCTG 540
Db 481 TGCAACTCCACAGCTAACACTGTGTGCGAGTTCATCTGTTTCAAAATCCAGAAACCGGCTG 540
Qy 541 TTCTCTACTGTTATCACCTTTGAGTGTGCTAATTGTGTCGGTGTGTTGCTTCGGTATCATTA 600
Db 541 TTCTCTACTGTTATCACCTTTGAGTGTGCTAATTGTGTCGGTGTGTTGCTTCGGTATCATTA 600
Qy 601 AGAAGATAAAGGTTCTACAGATGTTTTCTTAGCTTCCTTTTATGCTATGAAGTGATACT 660
Db 601 AGAAGATAAAGGTTCTACAGATGTTTTCTTAGCTTCCTTTTATGCTATGAAGTGATACT 660
Qy 661 ATGGAGGCAACTCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 720
Db 661 ATGGAGGCAACTCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 720
Qy 721 TTGAAGACCAAGCTGGCTCAAAATCACAGATCCAGACTCCAGACTAAGACAACCTCTAATAAGG 780
Db 721 TTGAAGACCAAGCTGGCTCAAAATCACAGATCCAGACTCCAGACTAAGACAACCTCTAATAAGG 780
Qy 781 AAACATTTAAATGGGACTGGCTTACAGTTCGGACGTTTTTGTCCATGATTAATCATAGTGG 840
Db 781 AAACATTTAAATGGGACTGGCTTACAGTTCGGACGTTTTTGTCCATGATTAATCATAGTGG 840
Qy 841 GAAGCATGGCAGCATCTAAGCAGACATGATGTTGGAGAAGGAGCTGAGATTTCTGCACTCT 900
Db 841 GAAGCATGGCAGCATCTAAGCAGACATGATGTTGGAGAAGGAGCTGAGATTTCTGCACTCT 900
Qy 901 TGATCTGCAAGCAATAAAGGAGACTGTGTCACACTATACACAGCTTGAACATAGGAG 960
Db 901 TGATCTGCAAGCAATAAAGGAGACTGTGTCACACTATACACAGCTTGAACATAGGAG 960
Qy 961 ACCTCAAAGCTGTCCCAAGTACAAACTTCTCTCAAGAGTCAATCTCTCTAATAA 1020
Db 961 ACCTCAAAGCTGTCCCAAGTACAAACTTCTCTCAAGAGTCAATCTCTCTAATAA 1020
Qy 1021 TACCAATTTCTATGAGGCAAGCATTTCAACACATGAGTCTATGAGGCGCAACCAATCA 1080
Db 1021 TACCAATTTCTATGAGGCAAGCATTTCAACACATGAGTCTATGAGGCGCAACCAATCA 1080
Qy 1081 AACCACACAGGTTAAACAATGGCCCTCTGACGCTCTCTGGTGGAGGCGCCCTCTTGAGAGT 1140
Db 1081 AACCACACAGGTTAAACAATGGCCCTCTGACGCTCTCTGGTGGAGGCGCCCTCTTGAGAGT 1140
Qy 1141 AAGTAACAATTTAGATGAAGGCAAGTCTCTGTATCAGGTCCTCAAAAGAACTCAGAGTAA 1200
Db 1141 AAGTAACAATTTAGATGAAGGCAAGTCTCTGTATCAGGTCCTCAAAAGAACTCAGAGTAA 1200
Qy 1201 TGGTCCACTGTGGTTCCCTATTAATACATGATGAGAAACATGACCTTACCTTACAGCTTCCA 1260
Db 1201 TGGTCCACTGTGGTTCCCTATTAATACATGATGAGAAACATGACCTTACCTTACAGCTTCCA 1260
Qy 1261 CCTCACTGACTTCCCTTCCCTAGCTTCTCAATCCAGAGTAAACCTCGCATTTTTCGGTA 1320
Db 1261 CCTCACTGACTTCCCTTCCCTAGCTTCTCAATCCAGAGTAAACCTCGCATTTTTCGGTA 1320
Qy 1321 ATGFGCCTCTCTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db 1321 ATGFGCCTCTCTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Qy 1381 TCTCCCACTCTCCACAGCCTCTCTTAAAGGCTGAATCAGTCTGTAGGTCATGTTTAAT 1440
```

```
Db 1381 TCTCCCACTCTCCACAGCCTCTCTTAAAGGCTGAATCAGTCTGTAGGTCATGTTTAAT 1440
Qy 1441 CTACTACTTTCTCTCTGCTCTGAGTCAATCAGATGTCTCTGGCTGAGCTCTCCCTCCTA 1500
Db 1441 CTACTACTTTCTCTCTGCTCTGAGTCAATCAGATGTCTCTGGCTGAGCTCTCCCTCCTA 1500
Qy 1501 TCTACAATAAAACCTTTCCCTTAAACAGAAATGCAAAAAA 1550
Db 1501 TCTACAATAAAACCTTTCCCTTAAACAGAAATGCAAAAAA 1550

RESULT 2
US-09-411-722-3
; Sequence 3, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501/040001
; CURRENT APPLICATION NUMBER: US/09/411.722
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)...(539)
US-09-411-722-3

Query Match 76.3%; Score 1182.4; DB 3; Length 1509;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 101; Indels 38; Gaps 4;

Qy 81 GCTGCTGCTGCTGCTGCTGAATCTGCCCTTTCGAGGTAAATTTGCTATGCTAGTAAT 140
Db 50 GTTCTCTTCTGCTGCTGCTGAATCTGTTCTTGGCGGTAAATTTGCTATGCTGTAATC 109
Qy 141 ACATCTCTTCAAAATGTCTCCGCTGCTGAATCTGTCTAAAGAGCTGTGTTGCAAGAACTG 200
Db 110 ATACTCTTCAACTGTCTCCGATGGTGAATACCACTCTAATGATGTCTGTTGCAAGACTG 169
Qy 201 TTCTGCAAGGTACATTTGTCAAGGCGCTTCGGAATCCCTCCATCTCAAGACAAATGTGA 260
Db 170 TCCCTCAGGTACATTTGTCAAGGCGCTTCGGAATCCCTCCATCTCAAGACAAATGTGA 229
Qy 261 GAAGTGTACCCAGGACATTTACAGAGAAGATTAATCTGATGCTGTGATACCTTTG 320
Db 230 GAAGTGTACCCAGGACATTTACAGAGAAGATTAATCTGATGCTGTGATGCTTTG 289
Qy 321 CTCCACTGTGATAAAGATCAGGAATGGTGGCGGCTGCTCAGCCACCAAGTACCGGAA 380
Db 290 CTCCACTGTGATAAAGATCAGGAATGGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 349
Qy 381 ATGCGAGTGCAGAACAGGTCTTTACTATATGACCCAAAAATTTCCAGAAATGCTGCGCGCC 440
Db 350 ATGCGAGTGCAGAACAGGTCTTTACTACTATGACCCAAAAATTTCCGGAATCATGCGCGCC 409
Qy 441 ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCAGCTTAACAC 500
Db 410 ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCAGCTTAACAC 469
Qy 501 TGTGTGAGTTCATCTGTTTCAAAATCCAGAAACCGGCTGTCTCTACTGTTATCACCTTT 560
Db 470 TGTGTGAGTTCATCTGTTTCAAAATCCAGAAACCGGCTGTCTCTACTGAT----- 520
```



```
QY 740 CAAATCACAGATCCAGACTACAGACAACTCTAATAAGGGAACATTTAATTGGGACTG 799
Db 674 CAAACTCACAGATCCGGACTAGGCACCTCTAATATAGGAAACATTTGAATTTGGGACTG 733
QY 800 GCTTACAGTTTCGGACGTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTAA 859
Db 734 GCTTACAGTTTCAGAGTTTGTCCATGATTATCATAGTGGGAAGCATGGAGGACCGAG 793
QY 860 GCAGACATGATGTTGGAGAGGAGCTGAGATTTCTGCATCTTGATCTGCAAGCAATAAAAA 919
Db 794 GCACACATGGTCTGGAGAGAAGCTGAGAGTTCTGCATCTTGATCTGCAAGCAATAAAA 853
QY 920 GGAGACTGTGGCCACACTATACACAGCTTGAAACATAGGAGACCTCAAAGCCTGCCCCA 979
Db 854 GGAGACTGTGGCCACACTATACATAGCTTGAAACATAGGAGACCTCAAAGCCTGCCCCA 913
QY 980 CAGTGACAACTTCTCCCAAGGTCATACCTCCTAATAATACCAATTTCTTATGAGGCA 1039
Db 914 CAGTGACAACTTCTCCCAAGGTCATACCTCCTAATAATACCAATTTCTTATGAGGCA 973
QY 1040 AGCAATCAACACATGATGTTATGAGGCGCAAAACCAATTCACACACAGGTTAAACA 1099
Db 974 AGCAATCAACACATGATGTTATGAGGCGCAAAACCAATTCACACACAGGTTAAACA 1033
QY 1100 TTGCCCTCTGAGCTCTCTGGTGGAGGCCCTCTTGGAGATGAATGATTAAGTAAAGTAA 1159
Db 1034 TTGCCCTCTGAGCTCTCTGGTGGAGGCCCTCTTGGAGATGAATGATTAAGTAAAGTAA 1093
QY 1160 GGCAAGTCTCTGGTATCAGGTCCAAAGAACTCAGGATGAATGATGATGTTGCTTCTTA 1219
Db 1094 GGCAAGTCTCTGGTATCAGGTCCAAAGAACTCAGGATGAATGATGATGTTGCTTCTTA 1153
QY 1220 TTAACATACATGAAGAACATGACCTCACCTTACAGCTCTCCACCTCACTGACTTCCCTTC 1279
Db 1154 TTAACATACATGAAGAACATGACCTCACCTTACAGCTCTCCACCTCACTGACTTCCCTTC 1213
QY 1280 CCTAGCTTCTCATTCACAGTAACCTGACCTGCAATTTTGGTAAATGTCCTTCTGGTCTT 1339
Db 1214 CCTAGCTTCTCATTCACAGTAACCTGACCTGCAATTTTGGTAAATGTCCTTCTGGTCTT 1273
QY 1340 CCTCTCTTCCCTCTCTTCTGGTCTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1399
Db 1274 CCTCTCTTCCCTCTCTTCTGGTCTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1333
QY 1400 CTCCTCTTAAGGCTGAATCAGTCTGAGTCAATGTTTAATCTACTACTTCTCTCTCTCT 1459
Db 1334 CGCCTCTAAGGCTGAGTCACTGAGTCAATGTTTAATCTACTACTTCTCTCTCTCTCT 1393
QY 1460 CTGGACTCATCCAGATCTCTGCTGAGCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT 1519
Db 1394 CTGGACTCATCCAGATCTCTGCTGAGCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT 1452
QY 1520 CCCTAACAGAAATGCAAAA 1539
Db 1453 CCCTAACAGAAATGGAACA 1472
```

RESULT 4

```
US-09-612-033B-9
; Sequence 9, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Saris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily
; TITLE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 9
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(552)
; OTHER INFORMATION: Primer 2086-39
US-09-612-033B-9
```

```
Query Match 38.8%; Score 602; DB 4; Length 702;
Best Local Similarity 93.6%; Pred. No. 1.2e-163;
Matches 657; Conservative 0; Mismatches 0; Indels 45; Gaps 1;
```

```
QY 1 TTGCACCTCGGCCCATGTTTGGCTTCTTCTGCAGCTTGGTCTCCAGTCTGAGTCTGCTGTTT 60
Db 1 TTGCACCTCGGCCCATGTTTGGCTTCTTCTGCAGCTTGGTCTCCAGTCTGAGTCTGCTGTTT 60
QY 61 CTTTGGCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 CTTTGGCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 AAATTTGCTATGCTAGAAATTACACTCTCTCAAATGTCGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 AAATTTGCTATGCTAGAAATTACACTCTCTCAAATGTCGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 GAGCTCTGTTTCAAGAACTGTTCTGCAGGTAACAATTTGTCAAGGCGCCCTCGGAAATCCCC 240
Db 181 GAGCTCTGTTTCAAGAACTGTTCTGCAGGTAACAATTTGTCAAGGCGCCCTCGGAAATCCCC 240
QY 241 CATACTCAAGGACAATGTGAGAGTGTCAACAGGAACTTCACAGAGAAAGATAATATAC 300
Db 241 CATACTCAAGGACAATGTGAGAGTGTCAACAGGAACTTCACAGAGAAAGATAATATAC 300
QY 301 CTGATGCTTGTATATCTTCTCCACTGTGATAAGATCAGGAAATGTTGGCGGACTGC 360
Db 301 CTGATGCTTGTATATCTTCTCCACTGTGATAAGATCAGGAAATGTTGGCGGACTGC 360
QY 361 TCAGCCACCAAGTACCGGAAATGCCAGTGTCCGAAACAGGCTTTTACTACTATGACCCAAA 420
Db 361 TCAGCCACCAAGTACCGGAAATGCCAGTGTCCGAAACAGGCTTTTACTACTATGACCCAAA 420
QY 421 TTTCCAGAAATCGTGGCGCCCATGTACCAAGTGTCCCAAGGAACTCCCTGCTCCAGGAA 480
Db 421 TTTCCAGAAATCGTGGCGCCCATGTACCAAGTGTCCCAAGGAACTCCCTGCTCCAGGAA 480
QY 481 TGCAACTCCACAGCTAACACTGTGTGAGTTCATCTGTTTCAA- 523
Db 481 TGCAACTCCACAGCTAACACTGTGTGAGTTCATCTGTTTCAAAGAGATCTGCTCAGTG 540
QY 524 -----ATCCAGAAACCGGCTGTTCCTTACTGTTATCA 555
Db 541 GCCTGGCCTATCTGAATGGTTTACAGAGATCCCAAGAAACCGGCTGTTCCTTACTGTTATCA 600
QY 556 CCTTTGAGTGTCTAAATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
Db 601 CCTTTGAGTGTCTAAATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 616 TACAGATGTTTCTTACGCTTCTCTTTTATTTGCTATGAAGTAT 657
Db 661 TACAGATGTTTCTTACGCTTCTCTTTTATTTGCTATGAAGTAT 702
```

RESULT 5

```
US-09-612-033B-13
; Sequence 13, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Saris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily
; TITLE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
```



```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,773B
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: DIAMOND=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3791 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-675-773B-3

Query Match      6.2%; Score 96.6; DB 3; Length 3791;
Best Local Similarity 69.7%; Pred. No. 5.5e-17;
Matches 189; Conservative 0; Mismatches 74; Indels 8; Gaps 4;

Qy 776 AAGGGAACATTTAATTGGGACTGGCTTACAGTTTCGGACGTTTTGTCCATGATTATCAT 835
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 265 AAGGGAACATTTAATTAGGGTCTGGCTTACAGTTTTCAGGAATTTAGTCCATCATGACGGA 206
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 836 AGTGGGAAGCATGCGCAGCATCTAAGCAGACATGATGTTGGAGAGGAGCTGAGATTCTTG 895
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 205 A--GGCAGGCTACCATGTCAGTAGGATGGATGCTGTGGAGAAG--GGAGACTTCTA 151
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 896 CATCTTGATCTGCAAGCAATAA--AAGGAGACTGTGTGCCACATATACACAGCTTGAAC 953
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 150 CATCTTGATCAAAATGCAGCCAGGAGAGGCTTTCATTCCACACTGGGCAGCTCATGAGC 91
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 954 ATAGGAGACCTCAAGCTGTCCCCACAGTCAGACAACTTCTCCAAAGGTCTATACCTC 1013
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 90 ATAGGAGACCTCAAGGCCAACCTCAAGTGACACACTTCTCTTAACACAGTCACA-CTC 32
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1014 CTAATAATACCATTTCTTTATGAGGCAAGCAT 1044
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
31 CTAACATGGCACTCCTTTGTGGGCCAAGCTT 1

RESULT 8
US-08-781-891-209
; Sequence 209, Application US/08/781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,891
; FILING DATE: 27-DEC-1996

;
; CURRENT APPLICATION DATA: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 240052.419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 209:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51259 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-781-891-209

Query Match      5.7%; Score 88.4; DB 3; Length 51259;
Best Local Similarity 68.9%; Pred. No. 6.5e-14;
Matches 182; Conservative 0; Mismatches 71; Indels 11; Gaps 4;

Qy 750 GAGATCCAGACTAAGCAACTCTTAAT-AAGGGAAACATTTAATTGGGACTGGCTTACAGT 808
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 809 TTCGGACGTTTTTCCATGATTATCATAGTGGGAAGCATGCGCAGCATCTTAAGCAGACATG 868
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3652 TTCAGAGGTTTGTGTCATTATCA-----TGGAAAGGCATGCGCAGTGTACAGGCAGACATG 3705
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 869 ATGTTTGAGAAGGAGCTGAGATTTCGATCTTTGATCTGCAAGCAATATAAAGGAGACTGT 928
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3706 GTGCTGGAGAAGGAGCTGAGATTTCATCCCATTTGGCGGCGCAGGAGGAGAGA--GA 3763
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 929 GTGCCACACTATACACAGCTTGAACATAGGAGACCTCAAAAGCCTGTCCCACAGTGACAA 988
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3764 GTGAGACACTGGTTGTGGCTTGAGCTTTTGACACCTCAAAGC--TCACATCTGCTGACAT 3821
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 989 ACTTCTCCCAACAAAGGTCACTACCT 1012
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3822 ACTTCTCCCAACAAAGGCCACCT 3845
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-618-166-209
; Sequence 209, Application US/09618166
; Patent No. 6583112
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/618,166
; FILING DATE: 17-Jul-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
```



```
; REFERENCE/DOCKET NUMBER: 240052.419C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 209:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51259 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 209:
US-09-618-166-209

Query Match          5.7%; Score 88.4; DB 4; Length 51259;
Best Local Similarity 68.9%; Pred. No. 6.5e-14;
Matches 182; Conservative 0; Mismatches 71; Indels 11; Gaps 4;

QY 750 GAGATCCAGACTAAGACAACCTTAAT--AAGGGAACATTAAATTGGGACCTGGCTTACAGT 808
Db 3592 GACACCATGACTACAGCACTCCGATAAGAAACAACTTTGATCAGGGCTGGCTTACCAG 3651
QY 809 TTGGAGCTTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTAAGCAGACATG 868
Db 3652 TTGAGAGTTTAGTCCATTATCA-----TGGAGGCGATGCGAGTGACAGGCGAGCATG 3705
QY 869 ATGTTGAGAGGAGCTGAGATTCTGCATCTTGATCTGCAAGCAATAAAGGAGACTGT 928
Db 3706 GTGCTGAGAGGAGCTGAGAGTTCTACATCCCAATTGGCGGGCAGGAGGAAGA--GA 3763
QY 929 GTGCCACACTATACAGCTTGACATAGAGAGACCTCAAGACCTGTGCTCCACAGTGACAA 988
Db 3764 GTGAGACACTGTTGTGGCTTGAGCTTTGACACCTCAAGC--TCATCTGGTGACAT 3821
QY 989 ACTTCTCCCAACAGGTCAACCT 1012
Db 3822 ACTTCTCCCAACAGGCCACACT 3845

RESULT 10
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; APPLICATION DATA:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29, 768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZ9pt-Fls
US-08-232-463-14

Query Match          5.5%; Score 85.2; DB 1; Length 7218;
Best Local Similarity 3.7%; Pred. No. 1.6e-13;
Matches 12; Conservative 216; Mismatches 94; Indels 0; Gaps 0;

QY 1202 GTCCCACTGGTTCCTATTAAACATCTACTGAAGAACATGACCTCACCTTACACGCTCTCCAC 1261
Db 1048 GGTGAGGAGCTTGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1107
QY 1262 CTCACTGACTTCCTTCCCTAGCTTCTCATTCACAGTAACCTGCATTTTGTGTAA 1321
Db 1108 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1167
QY 1322 TGTGCTTCTTGGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1381
Db 1168 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1227
QY 1382 CTCCCACTCTCCACAGCTCTCTCTTAAGGCTGAATCAGTCTGAGGTGATGTTTAAATC 1441
Db 1228 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1287
QY 1442 TACTACTTCTCTCTCTCTCTGAGCTCATCCAGATGTCTCTGGCTGAGCTCTCCCTCTCTAT 1501
Db 1288 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1347
QY 1502 CTACAATAAACCTTCCCTCT 1523
Db 1348 YYYYYYYYYYYYYYYYYYYY 1369

RESULT 11
US-09-657-346A-96
; Sequence 96, Application US/09657346A
; Patent No. 6503754
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
; FILE REFERENCE: RTS-0135
; CURRENT APPLICATION NUMBER: US/09/657,346A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 96
; LENGTH: 30310
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19791)...(19802)
; NAME/KEY: CDS
; LOCATION: (21160)...(21370)
; NAME/KEY: CDS
; LOCATION: (24168)...(24307)
; NAME/KEY: CDS
; LOCATION: (25696)...(25908)
; NAME/KEY: CDS
; LOCATION: (27235)...(27246)
US-09-657-346A-96
```

Query Match 5.3%; Score 81.4; DB 4; Length 30310;
 Best Local Similarity 75.5%; Pred. No. 5e-12;
 Matches 114; Conservative 0; Mismatches 36; Indels 1; Gaps 1;
 QY 755 CCAGACTAAGACAACTCTTAATAAGGGAACAACTTTAATTGGGACTGGCTTACAGTTTCGGA 814
 DB 22077 CCAGCCCAAGGCATCTTATTAAGGACAAATTTGGTTAGGCTGGCTTACAGTTTCAGA 22136
 QY 815 CGTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTTAAGCAGACATGATGTTG 874
 DB 22137 AGGTGAGTCCATTAAACATCATGGCAGGAAGCATGGCAGCGTCCAGGTAG-GATGGTGTG 22195
 QY 875 GAGAAGGAGCTGAGATTCTGTCATCTTGATC 905
 DB 22196 GAGGAAGAGCTGAGAGCTCTGTCATCTTGATC 22226

RESULT 12
 PCT-US93-12169-1/c
 ; Sequence 1, Application PC/TUS9312169
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: DNA SEQUENCE ENCODING OF THE CPG-1 NEURAL
 ; TITLE OF INVENTION: POLYPEPTIDE AND THE POLYPEPTIDE ENCODED THEREBY
 ; NUMBER OF SEQUENCES: 5
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/12169
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: IL 104097
 ; FILING DATE: 15-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: IL 106043
 ; FILING DATE: 16-JUN-1993
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Neimark, Sheridan
 ; REGISTRATION NUMBER: 20,520
 ; REFERENCE/DOCKET NUMBER: CITRI=2 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3872 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 505..786
 PCT-US93-12169-1

Query Match 5.1%; Score 78.6; DB 5; Length 3872;
 Best Local Similarity 68.8%; Pred. No. 8.9e-12;
 Matches 170; Conservative 0; Mismatches 64; Indels 13; Gaps 4;
 QY 783 ACATTTAATTGGGACTGGCTTACAGTTTCGAGCGTTTGGTCCATGATTATCATAGTGGGA 842
 DB 3862 ACATTTAATTGAAGTTGGCTTACAGGTTTACAGGTTTACAGGTTTACAGTATGATCATGATCAAGGTGGGA 3803

QY 843 AGCATGGCAGCATCTTAAGCAGACATGATGTTGGAGAAGGAGCTGAGATTTTCGATCTTG 902
 DB 3802 A-CATGGCAGGACCCAGGCGAGCATGGTGC---AGAAGGAGCTGAGAGTTTCTACATCTTC 3747
 QY 903 ATCTGCAAGCAATAAAGGAGAGCTGTGTGCCACACTATACACAGCTTGAACATAGGAGAC 962
 DB 3746 ATCTGAAGC-----TGCTAGCAGATACTGACTTCCAGGCGAGCTAGGACAAGGG--T 3696
 QY 963 CTCAAAGCCTGTCCCAACAGTCAGCAAACTTCTCTCCAAAGGTCATACCTCTCTTAATAATA 1022
 DB 3695 ATTAAGSCCTACACCCACAGTCAGACACCTTACTTCCAAAGGCCACACCTCTTAAAGATG 3636
 QY 1023 CCATTTTC 1029
 DB 3635 CCACCTTC 3629

RESULT 13
 US-08-477-831C-7
 ; Sequence 7, Application US/08477831C
 ; Patent No. 6429291
 ; GENERAL INFORMATION:
 ; APPLICANT: TURLEY, EVA A.
 ; APPLICANT: SHUEN, ZHANG
 ; APPLICANT: ENTWISTLE, JOYCELYN
 ; TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FISH & NEAVE
 ; STREET: 1251 AVENUE OF THE AMERICAS
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10020-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Rel. #1.0, ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,831C
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PIERRE, MARGARET A.
 ; REGISTRATION NUMBER: 30,709
 ; REFERENCE/DOCKET NUMBER: SIM-10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-596-9000
 ; TELEFAX: 212-596-9090
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4243 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; DESCRIPTION: /desc = "Intron 2"
 US-08-477-831C-7

Query Match 4.8%; Score 74.2; DB 3; Length 4243;
 Best Local Similarity 70.6%; Pred. No. 1.8e-10;
 Matches 142; Conservative 0; Mismatches 53; Indels 6; Gaps 3;
 QY 900 TTGATCTGCAAGCAATAAAGGAGAGACTGTGTGCCACACTATACACAGCTTGAACATAGGA 959
 DB 32 TAGATCCACAGCGCAGCAAAAGGAGAC--TGTGCCACACTAGGCTTAAGCTTGAAGCTTATAA 89
 QY 960 GACCTCAAGCCTGTGCCACAGTCAGCAAACTTCTCTCCAAAGGTCATACCTCTCTTAATA 1019
 DB 90 AACCTCAAAATCCCAACCTCCACAGTCAGCACACTTCTTCCAAAGGCCA---CCCTTAATA 146
 QY 1020 ATACCATTTCTTATGAGGCAAGCAATTCAAACACATGAGTCTATGAGGGCCCAACCAATTC 1079

Db 147 ATGCCATCCCTGGGCCAAGTA-TCAAACACACAGAGTCTCTGAGGSCCATTTACTATCA 205
Qy 1080 AAACACCACACAGGTTTACAAT 1100
Db 206 AACCTCCACCGTATCAAACT 226

RESULT 14

US-09-917-254-47/c
; Sequence 47, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 5257
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-917-254-47

Query Match 4.8%; Score 74.2; DB 4; Length 5257;
Best Local Similarity 71.6%; Pred. No. 2e-10;
Matches 111; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

Qy 771 CTAATAAGGGAACATTTAATTTGGGACTGGCTTACAGTTTCGGACGTTTGTCCATGATT 830
Db 5256 CTATAAGGAAGACATTTAATTTGGGCTGCTTACAG-TTCAGAGCTTCAGTCAATTATT 5198
Qy 831 ATCATAGTGGAGCAGTGGCAGCATCTAAGCAGACATGATGTTGGAGAGGAGCTGAGAT 890
Db 5197 GTCATGTTGGAGGATGGCAGCATGCGAGTACATCATTTCCAGGAGAGCAGCAGAGAG 5138
Qy 891 TTCTGCATCTTGCTCGACCATATAAGGAGAC 925
Db 5137 TTCTACATCAGATTGGCAGGCTATGATCAGGGAC 5103

RESULT 15

US-09-245-041-5
; Sequence 5, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 90050
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-245-041-5

Query Match 4.8%; Score 74; DB 3; Length 90050;
Best Local Similarity 76.9%; Pred. No. 1.3e-09;
Matches 103; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

Qy 771 CTAATAAGGGAACATTTAATTTGGGACTGGCTTACAGTTTCGGACGTTTGTCCATGATT 830
Db 47238 CTCTTACGAAGGACATTTAATTTGGGCTGCTTACAGTTTTCAGAGGTTTAAATCCATATC 47297
Qy 831 ATCATAGTGGAGCAGTGGCAGCATCTAAGCAGACATGATGTTGGAGAGGAGCTGAGAT 890
Db 47298 ATCATGCGCAGGAAGCATGGCAGCATTCAGGCAGATGTGGTCTGGAGGAGCCG-AGAGAG 47356
Qy 891 TTCTGCATCTTGAT 904
Db 47357 TTCTATATCTTGAT 47370

Search completed: September 9, 2005, 07:09:09
Job time : 783.13 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 16:10:01 ; Search time 3520.54 Seconds
(without alignments)
2891.383 Million cell updates/sec

Title: US-10-622-407-7
Perfect score: 1550
Sequence: 1 ttgactggccatgttgg.....aatgcaaaaaaaaaaaaaa 1550

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 7351250 seqs, 323620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1550	100.0	1550	17	US-10-622-407-7 Sequence 7, Appli
2	1182.4	76.3	1509	9	US-09-855-266A-3 Sequence 3, Appli
3	1182.4	76.3	1509	19	US-10-802-332-3 Sequence 3, Appli
4	709.4	45.8	967	14	US-10-193-616-7 Sequence 7, Appli
5	602	38.8	702	17	US-10-622-407-9 Sequence 9, Appli
6	514.6	33.2	1200	17	US-10-622-407-13 Sequence 13, Appli
7	412	26.6	412	17	US-10-622-407-5 Sequence 5, Appli

8	392	25.3	415	9	US-09-728-445-737 Sequence 737, App
9	392	25.3	415	22	US-10-964-549-737 Sequence 737, App
10	253.2	16.3	357	14	US-10-193-616-5 Sequence 5, Appli
c 11	205.6	13.3	124289	13	US-10-087-192-817 Sequence 817, App
12	191.6	12.4	203070	13	US-10-087-192-247 Sequence 247, App
13	187.6	12.1	721377	21	US-10-461-862-163 Sequence 163, App
14	197	12.1	111836	21	US-10-322-281-51 Sequence 51, Appli
15	186	12.0	16940	22	US-10-942-954-2 Sequence 2, Appli
16	182.2	11.8	35425	19	US-10-322-696-91 Sequence 91, Appli
17	178.2	11.5	71057	13	US-10-087-192-409 Sequence 409, App
18	168.6	10.9	56587	13	US-10-087-192-1687 Sequence 1687, Ap
19	167.4	10.8	27299	13	US-10-087-192-937 Sequence 937, App
20	166.4	10.7	134442	21	US-10-461-862-23 Sequence 23, Appli
c 21	166.2	10.7	121129	19	US-10-322-281-587 Sequence 587, App
c 22	164	10.6	203070	13	US-10-087-192-247 Sequence 247, App
23	161.4	10.4	150351	19	US-10-322-281-453 Sequence 453, App
c 24	160.8	10.4	151858	19	US-10-322-281-653 Sequence 653, App
c 25	159.6	10.3	51281	11	US-09-997-722-139 Sequence 139, App
26	158.6	10.2	29222	17	US-10-085-117-349 Sequence 349, App
c 27	154.8	10.0	117382	13	US-10-087-192-1435 Sequence 1435, Ap
c 28	154.8	10.0	659158	9	US-09-771-208-20 Sequence 20, Appli
c 29	154	9.9	89756	21	US-10-461-862-133 Sequence 133, App
c 30	153.6	9.9	122859	13	US-10-087-192-37 Sequence 37, Appli
c 31	150.6	9.7	65253	17	US-10-085-117-331 Sequence 331, App
c 32	150.6	9.7	185555	13	US-10-087-192-1999 Sequence 1999, Ap
c 33	150.4	9.7	37923	21	US-10-087-192-1891 Sequence 1891, Ap
34	149	9.6	1900	21	US-10-764-420-905 Sequence 905, App
35	146.6	9.5	219715	20	US-10-417-375-63 Sequence 63, Appli
36	146.4	9.4	45736	19	US-10-322-281-767 Sequence 767, App
c 37	146	9.4	54669	11	US-10-322-281-347 Sequence 347, App
c 38	145.6	9.4	41637	11	US-09-997-722-103 Sequence 103, App
c 39	144.4	9.3	66499	19	US-10-322-281-39 Sequence 39, Appli
c 40	143.2	9.2	38142	20	US-10-417-375-55 Sequence 55, Appli
c 41	142.4	9.2	63502	13	US-10-087-192-271 Sequence 271, App
c 42	142.4	9.2	177249	17	US-10-085-117-223 Sequence 223, App
c 43	142	9.2	57561	13	US-10-087-192-1129 Sequence 1129, Ap
c 44	141.8	9.1	608916	21	US-10-461-862-1 Sequence 1, Appli
c 45	140	9.0	38977	13	US-10-087-192-1321 Sequence 1321, Ap

ALIGNMENTS

RESULT 1
US-10-622-407-7
; Sequence 7, Application US/10622407
; Publication No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US/10/622,407
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US 09/612,033
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(606)
; FEATURE:
; OTHER INFORMATION: mouse tmst2
US-10-622-407-7

Query Match 100.0%; Score 1550; DB 17; Length 1550;
Best Local Similarity 100.0%; Pred. No. 0;


```
QY 201 TTCTGCAGGTACATTTGTCAAGGGCCCTCGGAAATCCCCCATACTCAAGGACAATGTGA 260
D 170 TCCCTCAGGTACATTTGTCAAGGGCCCTCGGAAATCCCCCATACTCAAGGACAATGTGA 229
QY 261 GAAGTGTCAACCCAGGAACATTTACAGAGAAGATAAATTAAGTGTCTGTATACATTTG 320
D 230 GAAGTGTCAACCCAGGAACATTTACAGAGAAGATAAATTAAGTGTCTGTATACATTTG 289
QY 321 CTCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGTCTAGCCACCAAGTACCGGAA 380
D 290 CTCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGTCTAGCCACCAAGTACCGGAA 349
QY 381 ATGCCAGTGGCAACAGTCTTTACTACTATGACCCGAAATTTCCAGAAATCGTGGCGCCC 440
D 350 ATGCCAGTGGCAACAGTCTTTACTACTATGACCCGAAATTTCCGGAATCATGGCGCCC 409
QY 441 ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATCAACTCCACAGCTAACAC 500
D 410 ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATCAACTCCACAGCTAACAC 469
QY 501 TGTGTGAGTTCATCTGTTTCAATCCAGAAACCGGCTGTCTCTACTGTATACACCTTT 560
D 470 TGTGTGAGTTCATCTGTTTCAATCCAGAACTGGCTGTCTCTACTGAT----- 520
QY 561 GAGTGTGCTAATTTGTGTCTGTTTCCGTTATCATTAAGAAATAAAGGTTCTACAG 620
D 521 -----GCTAATTTGTCTGTTTCTGTTATCTGAAGAAGATAAAGGTTCTACAG 562
QY 621 ATGTTTCT--TAGCTTCTTTTATTTGATGAGTGTATCTATGAGGCAACTCTTTAT 679
D 563 ATGTTGTTCTTTAGCTTCTTTTATTTGTTGTAAGAAACCAATGAGGCAACTCT-- 617
QY 680 TTTATTTATTTTATTTTATTTTAAATGTTGATTTGAAGACCAAGGCTGGCCT 739
D 618 ----TTCAATTTTATTTTAAATGTTGTTGAACTTTGAACTTTGAAGACCAAGGCTGGACT 673
QY 740 CAAATCAGAGATCCAGACTAAGACAATCTTAATAAGGAAACAATTAATTTGGGACTG 799
D 674 CAAACTCAGAGATCCGACTAGGCACCTTAATAATAGGAAACAATTAATTTGGGACTG 733
QY 800 GCTTTACAGTTTCGACGCTTTGTCATGATATCATAGTGGGAGCATGCGACATCTAA 859
D 734 GCTTTACAGTTTCGACGCTTTGTCATGATATCATAGTGGGAGCATGCGGACGAG 793
QY 860 GCAGACATGATTTGGAGAGGAGCTGAGATTTCTGCATCTTGATCTGCAAGCAATAAAA 919
D 794 GCACACATGTTGTTGAGAGAGAGCTGAGATTTCTGCATCTTGATCTGCAAGCAATAAAA 853
QY 920 GGAGACTGTGTGCACACTATACACAGCTTTGAACATAGGAGACTCAAGCCTGTCCCA 979
D 854 GGAGACTGTGTGCACACTATACACAGCTTTGAACATAGGAGACTCAAGCCTGTCCCA 913
QY 980 CAGTGACAAATTCCTCCACAAAGGTCTACCTCTTAATAATACCAATTTCTATGAGCA 1039
D 914 CAGTGACAAATTCCTCCACAAAGGTCTACCTCTTAATAATACCAATTTCTATGAGCA 973
QY 1040 AGCAATCAAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCAACAGGTTAACAA 1099
D 974 AGCAATCAAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCAACAGGTTAACAA 1033
QY 1100 TTGCCCTCTCAGCTCTCTGTGTGAGGCCCTCTCTTGAAGATGAAGTAAACAATTTAGATGAA 1159
D 1034 TTGCCCTCTCAGCTCTCTGTGTGAGGCCCTCTCTTGAAGATGAAGTAAACAATTTAGATGAA 1093
QY 1160 GGCAGTCTCTGTTATCAGGTCCAAAGAAACTCAGGATGAATGGTCCACTGTGGTCTTA 1219
D 1094 GGCAGTCTCTGTTATCAGGTCCAAAGAAACTCAGGATGAATGGTCCACTGTGGTCTTA 1153
QY 1220 TTAACATACCTGAAGAAACATGACCTTACAGCTCTCCACCTCAGTCTGCTCCCTTCC 1279
D 1154 TTAACATACCTGAAGAAACATGACCTTACAGCTCTCCACCTCAGTCTGCTCCCTTCC 1213
```

```
QY 1280 CCTAGCTTCTCATTTCCAGGTAACCTGCGCATTTTTTGGTAATGTGCTCTTGGTTCTT 1339
D 1214 CCTAGCTTCTCATTTCCAGGTAACCTGCGCATTTTTTGGTAATGTGCTCTTGGTTCTT 1273
QY 1340 CCTCTCTTTTCCCGCTCTCTTTCTGGTCTTTACTTCTCTCTCTCCCTCCACCTCCACCAGC 1399
D 1274 CCTCTCTTTTCCCGCTCTCTTTCTGGTCTTTACTTCTCTCTCTCCCTCCACCTCCACCAGC 1333
QY 1400 CTCTCTTTAAGGCTGAATCAGTCTGTAGTGTCAATGTTTAACTACTACTTCTCTCTGCT 1459
D 1334 CGCTCTTTAAGGCTGAGTCTGTCAGGCCATGTTTAACTACTACTTCTCTCTGCT 1393
QY 1460 CTGCACTCTACAGATGTCTCTGCTGAGCTCTCCCTCTCTATCTACAAATAAAACCTCTCC 1519
D 1394 CTGCACTCTACAGATGTCTCTGCTGAGCTCTCCCTCTCTATCTACAAATAAA--CCTTCC 1452
QY 1520 CCCTAACCAAGAAATGCAAAA 1539
D 1453 CCCTAACCAAGAAATGGAACA 1472

RESULT 3
US-10-802-332-3
; Sequence 3, Application US/10802332
; Publication No. US20040152879A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/10/802,332
; PRIOR FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: US/09/855,266
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)...(539)
US-10-802-332-3

Query Match 76.3%; Score 1182.4; DB 19; Length 1509;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 101; Indels 38; Gaps 4;

QY 81 GCTGTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAAGTAAATTTGCTATGCTAGAAATT 140
D 50 GTTCTCTTGTGCTGCTGCTGAATCTGTTCTTGGCGGTAAATATTTGCTATGCTGAATC 109
QY 141 ACACCTCTTCAATGTCCTGCTGCTGAATCTGCTCTAAAGAGCTGCTGTTGCAAGACTG 200
D 110 ATACTCTTCACTGTCCTGCTGCTGAATCTGAATACCACTCTAATGATGTCTGTTGCAAGACTG 169
QY 201 TTCTGCAAGGTACATTTTGTCAAGGCGCTCGGAAATCCCCCATACTCAAGGACAATGTGA 260
D 170 TCCTCAGGTACATTTTGTCAAGGCGCTCGGAAATCCCCCATACTCAAGGACAATGTGA 229
QY 261 GAAGTGTCAACCCAGGAACATTTCAAGAGAAGATAAATTAAGTGTCTGTATACATTTG 320
D 230 GAAGTGTCAACCCAGGAACATTTCAAGAGAAGATAAATTAAGTGTCTGTATGAACTTTG 289
QY 321 CTCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGTCTAGCCACCAAGTACCGGAA 380
```


Db 190 CTGATGCTTGTATATCTTTGCTCACCCTGTGATTAAGATCAGGAATGGTGGCGACTGC 249
Qy 361 TCAGCCACCAAGTACCGGAATGCGAGTGCAGAACAGGTCTTTACTACTATGACCCAAAA 420
Db 250 TCAGCCACCAAGTACCGGAATGCGAGTGCAGAACAGGTCTTTACTACTATGACCCAAAA 309
Qy 421 TTTCAGAAATCGTGGCGCCCATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAA 480
Db 310 TTTCAGAAATCGTGGCGCCCATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAA 369
Qy 481 TGAACCTCCACAGCTAACACTGTGTGAGTTCATCTGTTTCAAA 524
Db 370 TGAACCTCCACAGCTAACACTGTGTGAGTTCATCTGTTTCAAA 413

RESULT 9
US-10-964-549-737
; Sequence 737, Application US/10964549
; Publication No. US2005018667A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Mutated Mammalian Cells and Animals
; FILE REFERENCE: LEX-0286-USA
; CURRENT APPLICATION NUMBER: US/10/964,549
; PRIOR FILING DATE: 2004-10-13
; PRIOR APPLICATION NUMBER: US/09/750,456
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/728,445
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/169,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 737
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-964-549-737

Query Match 25.3%; Score 392; DB 22; Length 415;
Best Local Similarity 99.8%; Pred. No. 7.3e-98;
Matches 403; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 121 AAATTTGCTATGCTAGAAATACACTCTCTCAATGTCCCGTGTGTAATCTGTCTTAAA 180
Db 11 AAATTTGCTATGCTAG-ATTACACTCTTCAATGTCCCGTGTGTAATCTGTCTTAAA 69
Qy 181 GACGTCTGTTGCAAGAACTGTTCTGAGGTACATTTGTCAAGGCGCCCTCGAAATCCCC 240
Db 70 GACGTCTGTTGCAAGAACTGTTCTGAGGTACATTTGTCAAGGCGCCCTCGAAATCCCC 129
Qy 241 CATACTCAAGACAATGTGAGAGTGTACCCAGGAACATTCACAGAGAAAGATAATTAC 300
Db 130 CATACTCAAGACAATGTGAGAGTGTACCCAGGAACATTCACAGAGAAAGATAATTAC 189
Qy 301 CTGGATGCTGTATATCTTTGCTCCACCTGTGATTAAGATCAGGAATGGTGGCGACTGC 360
Db 190 CTGGATGCTGTATATCTTTGCTCCACCTGTGATTAAGATCAGGAATGGTGGCGACTGC 249
Qy 361 TCAGCCACCAAGTACCGGAATGCGAGTGCAGAACAGGTCTTTACTACTATGACCCAAAA 420
Db 250 TCAGCCACCAAGTACCGGAATGCGAGTGCAGAACAGGTCTTTACTACTATGACCCAAAA 309
Qy 421 TTTCAGAAATCGTGGCGCCCATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAA 480
Db 310 TTTCAGAAATCGTGGCGCCCATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAA 369
Qy 481 TGAACCTCCACAGCTAACACTGTGTGAGTTCATCTGTTTCAAA 524
Db 370 TGAACCTCCACAGCTAACACTGTGTGAGTTCATCTGTTTCAAA 413

RESULT 10
US-10-193-616-5
; Sequence 5, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymz5, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)..(356)
US-10-193-616-5

Query Match 16.3%; Score 253.2; DB 14; Length 357;
Best Local Similarity 87.9%; Pred. No. 2.1e-59;
Matches 276; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 81 GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGCTATGCTAGAAATT 140
Db 44 GTTCCTCTTGTGCTGCTGCTGAATCTGTTCTTCCGGTAATATTTGCTATGCTGAATC 103
Qy 141 ACATCTCTTCAAAATGTCCCGTGTGTAATCTGTTCAAGAGCTGTTGCAAGAACTG 200
Db 104 ATACTCTTCAACTGTCCCGATGTTGAATACCACTCTAATGATGTCTGTTGCAAGAACTG 163
Qy 201 TTCTGCAGGTACATTTGTCAAGGCGCCCTCGAAATCCCCCATACTCAAGACAATGTGA 260
Db 164 TCCTCAGGTACATTTGTCAAGGCGCCCTCGAAATCCCCCATACTCAAGACAATGTGA 223
Qy 261 GAAGTGTACCCAGGAACATTCACAGAGAAAGATAATTACTGGATGCTTGTACTTTG 320
Db 224 GAAGTGTACCCAGGAACATTCACAGGAAGATAATGGCTGCTGATGATTGTGAACCTTG 283
Qy 321 CTCACCTGTGATAAAGATCAGGAATGTGGCGGACTGCTCAGCCACCAAGTACCCGAA 380
Db 284 CTCACCTGTGATAAAGACCAAGATAATGGTGGCTGACTGTTCTGCCACCAGTACCCGAA 343
Qy 381 ATGCCAGTGCAGAA 394
Db 344 ATGCCAGTGCAGAA 357

RESULT 11
US-10-087-192-817/c
; Sequence 817, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02

```
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 817
; LENGTH: 124289
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(124289)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-817
```

```
Query Match 13.3%; Score 205.6; DB 13; Length 124289;
Best Local Similarity 75.3%; Pred. No. 8.9e-45;
Matches 256; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 755 CCAGCTAAGACAACTCTAATAAGGGAACATTTAATTGGGACTGGCTTACAGTTTCGGA 814
Db 32622 CCAGGCTGACAACTTTTATAAAGAAACATTTAACTGGGAATGGCTTACAGTTTCGA 32563

Qy 815 CGTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTTAAGCAGACATGATGTTG 874
Db 32562 AGTTTAGTCCATTATCATATGGCAGGAAGCATGGCAGTATCCAGGCAGAAATGGTGTG 32503

Qy 875 GAGAAGGAGCTGAGATTCTGCATCTTGATCTGCAAGCAATAAAGGAGAGCTGTGCGCA 934
Db 32502 GAGAAGGAGTTTGACAGTTCTTACATATTGATCTGAAGGCAGCAGAAAGGGGATTGTGTTCCA 32443

Qy 935 CACTATATACAGCTTGAACATAGAGACCTCAAAAGCCTGTCCCAAGTGCACAACTTCC 994
Db 32442 CACTGGTGGAGCTTGACATAGAGGCTTAAAGCTTGTCTTCAATGATACATTTCT 32383

Qy 995 TCCAAACAGGTATACCTCTCTTAATAATACCAATTTCTTATAGGGAAGCATTTCAACACAT 1054
Db 32382 TCCAAATATGTTCTCACCTCTCTTAATAATGCTACTCCCTATGGGCCAAACATTTCAAAGACAT 32323

Qy 1055 GAGTCTATAGGGGCCAAACCAATTTCAACACACACAGTTT 1094
Db 32322 GATTCTATAAGGGGTACATACCTATTTCAGAGCACCACAGATT 32283
```

```
RESULT 12
US-10-087-192-247
; Sequence 247, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 247
; LENGTH: 203070
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(203070)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-247
```

```
Query Match 12.4%; Score 191.6; DB 13; Length 203070;
Best Local Similarity 75.4%; Pred. No. 8.9e-41;
Matches 264; Conservative 0; Mismatches 84; Indels 2; Gaps 2;
```

```
Qy 747 ACAGAGATCCAGACTAAGACAACTCTAAT-AAGGGAACATTTAATTGGGACTGGCTTAC 805
Db 97220 AGAGACACCTTGACCATGGCAACTCTTATAAGGAAACATTTAACTGGGGCTGGCTTAT 97279

Qy 806 AGTTTCGGACGTTTGTGCCATGATTATCATAGTGGGAAGCATGSCAGCATCTAAGCAGAC 865
Db 97280 AG-TTCAGAGGTTTAGTTTCATTCATCATGACAGGAGCCAGACAGCATGCGGCGAGAC 97338

Qy 866 ATGATGTTGGAGAAGGAGCTGAGATTTTCTGCATCTTTCATCTGCAAGCAATAAAGGAGAC 925
Db 97339 ATGGTGTCTGGGGAGAGCTGAGAGTTTCTACATCTGGATCCACAGACAAGCAGCAAAAG 97398

Qy 926 TGTGTGCCACACTATACAGCTTGAACATAGAGAGCCTCAAAGCCTGTCCCCACAGTGA 985
Db 97399 AGACTGTCTACACTAGGCTTGACTTGAGCATCTAAGACCTCAAAGCCCAACCCACAGTGA 97458

Qy 986 CAAACTTCTCCCAACAAAGGTCATACCTCTTAATAATACCAATTTCTTATGAGGCAAGCAT 1045
Db 97459 CACACTTCTCCCAACAAAGCCACCTCTTAATAGTGCCACTTCTATGAGCCAGCAT 97518

Qy 1046 CAAACACATGAGTCTATGAGGGCCAAACCAATTTCAAACCCACAGGTGA 1095
Db 97519 CAAACACATGAGTCTTTTGGGGCTATACCTATTCAAACCAACACAAATATA 97568
```

```
RESULT 13
US-10-461-862-163
; Sequence 163, Application US/10461862
; Publication No. US20050090434A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001800
; CURRENT APPLICATION NUMBER: US/10/461,862
; CURRENT FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 721377
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(721377)
; OTHER INFORMATION: n = A,T,C or G
US-10-461-862-163
```

```
Query Match 12.1%; Score 187.6; DB 21; Length 721377;
Best Local Similarity 77.8%; Pred. No. 2.3e-39;
Matches 252; Conservative 0; Mismatches 69; Indels 3; Gaps 2;

Qy 747 ACAGAGATCCAGACTAAGACAACTC-TAATAAGGGAACATTTAATTGGGACTGGCTTAC 805
Db 193445 AGAGACACCATGACCATGGCACTCTTAAAAGGAAGCATTTCAATTGGGGCTGGCTTAC 193504

Qy 806 AGTTTCGGACGTTTGTGCCATGATTATCATAGTGGGAAGCATGSCAGCATCTAAGCAGAC 865
Db 193505 AGTTTCTGAGGTTTAGTCCATTTATATATAGCAGGAACATGCGCAGCATGCAAGCCAAC 193564

Qy 866 ATGATGT--TGGAGAGGAGCTGAGATTCTTGATCTTGATCTGCAAGCAATAAAGGAG 923
Db 193565 ATGGTGTGCTGAAGAGGAGTTGAGAGTTCTTATATCTTTATCCACAGGCAACAGAGAG 193624

Qy 924 ACTGTGTGCCACACTATACACAGCTTGAACATAGGAGACCTCAAAGCCTGTGCCACAGT 983
Db 193625 ACTATAGCCACACTGGGCATTAAGTGGACATGAGACATTAAGAGCTGCCCCCAACAGT 193684

Qy 984 GACAACTTCTCCCAACAAAGGTCTATCTCTTAATAATACATTTCTTATGAGGCAAGCA 1043
Db 193685 GACATTTCTTTCAACAAAGGCGACACCTCTTAATAGTGCCACTCTCTATGCGCCAAAGCA 193744

Qy 1044 TTCAACACATGAGTCTATGAGGG 1067
```

```
Db 193745 TTCAACATATGAGTCTAAGGGG 193768
||||| ||||||| ||||||| |||
RESULT 14
US-10-322-281-51
; Sequence 51, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 111836
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(111836)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-51

Query Match 12.1%; Score 187; DB 19; Length 111836;
Best Local Similarity 78.8%; Pred. No. 1.2e-39;
Matches 223; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 789 AATTGGGACTGGCTTACAGTTTCGGAGCTTTGTCATGATTTCTGATCTGCTGC 908
Db 56881 AATTGGGCTGGCTTACAGTTTCAGAGATTTCAGTCCATTATCATCATCGTAGGAAGTATG 56940

Qy 849 GCAGCATCTAAGCAGACATGATGTTGGAGAGGAGCTGAGATTTCTGATCTGCTGC 908
Db 56941 GTAGCATCCAGGCAGACATGTTGTCGACAAAGGGGCTAAGAGTTCTATATCTTGATCCAT 57000

Qy 909 AAGCAATAAAGGAGACTGTTGTCACATATACACAGCTTGAACATAGGAGACTCAAA 968
Db 57001 AGGCAGCAGAGGGGACTGTATACCACTGGGTGAGCTTGAGCATAGGAGATCTCAA 57060

Qy 969 GCCTGTCCCACTGAGTCAAACTTCCTCCAAAGGCTCATACCTCTTAATAATACCAATTT 1028
Db 57061 GCCCAACTCCCAATGACACATCTCTCCAAAGGCGCACACCTCTTAATAGTACCACCTT 57120

Qy 1029 CTTATGAGGCAGCATTTCAACACATGATCTATGAGGGCCAA 1071
Db 57121 CTTGAGGCAGCATTTCAACACAGGAGTTTGTGGAGGCCAA 57163

RESULT 15
US-10-942-954-2
; Sequence 2, Application US/10942954
; Publication No. US20050144662A1
; GENERAL INFORMATION:
; APPLICANT: BML, INC.
; APPLICANT: Masataka NAKAMURA
; APPLICANT: Kazuo SUGAMURA
; APPLICANT: Shoichi TAKANO
; APPLICANT: Kinya NAGATA
; APPLICANT: Hiroyuki HIRAI
; TITLE OF INVENTION: KNOCKOUT MOUSE
; FILE REFERENCE: Q83632
; CURRENT APPLICATION NUMBER: US/10/942,954
; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: JP 2003-328480
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 16940
```

```
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)...(6)
; OTHER INFORMATION: n is a, c, g, or t
US-10-942-954-2

Query Match 12.0%; Score 186; DB 22; Length 16940;
Best Local Similarity 76.3%; Pred. No. 8e-40;
Matches 255; Conservative 0; Mismatches 75; Indels 4; Gaps 2;

Qy 750 GAGATCCAGACTAAGACAACCTCTAATAAGGGAACATTTAATTGGGACTGGCTTACAGTT 809
Db 2767 GACACCATGACCTGGGTAATTTTCATAAAGAAACATTTAATTGGTACTGGCTTACAGTT 2826

Qy 810 TCGGAGCTTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTAAGCAGACATGA 869
Db 2827 TCAGAGGTCTAGTCCATTATTGCCATGTTAGGA--CATAGTGGCATGCAGGCAGACAGA 2884

Qy 870 TGTTGGAGAAGGAGCTGAGATTTCTGCATCTTGCATCTTGCAGCAATAAAGGAGACTGTG 929
Db 2885 TGCTGGAGAAGGAGCTGAGAGTTCTTACATCTTGATCCAAAGTCAGCAGAAGGAGACTGTG 2944

Qy 930 TGCCACACTATACACAGCTTGAACATAGGAGACCTCAAGCCCTGTCCCCACAGTGACAA 989
Db 2945 TGCCACACTGGGTGTAGCTTGGAGCATAGGAGACCTCAAGCCCTGTCCCCACAGTGACAA 3004

Qy 990 CTTCTCTCCAAAGGTCATACCTCTTAATAATACCAT--TTCTTATGAGGCAAGCATTTCA 1047
Db 3005 TTTCTCTCCAAAGGCCATACCTACTACTAGTGTCTATCTCCCTATGGGTCAAGCATTTCA 3064

Qy 1048 AACACATGAGTCTATGAGGGCCAAACCAATTTCAA 1081
Db 3065 AACACTTGAGTCTATGGGGTCATTTCTCTTTTAA 3098
```

Search completed: September 9, 2005, 08:34:38
Job time : 3525.54 secs

THIS PAGE BLANK (USPTO)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.
 Web site: <http://genome.uiowa.edu>
 Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
 Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,
 Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,
 Scheetz, T., Smith, C., Smith, E., Tack, D., Trout, K., Walters, J.,
 Casavant, T., Soares, M.B.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: Plate: Row: Column: 0
 This clone has the following problem: clone inconsistent with known
 gene structure.

FEATURES

source

Location/Qualifiers
 1. 4224
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30652769"
 /tissue_type="Eye"
 /clone_lib="NIH_BMAP_HBO"
 /lab_host="DH10B"
 /note="Vector: pYX-ASC"

ORIGIN

Query Match 98.2%; Score 1521.8; DB 3; Length 4224;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1535; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 1 TTGCACCTCGGCGCATGTTGGCTTCTTCGACGTTGGTGCACGTCGAGTCGCTGTTTC 60
 Db 10 TTGCACCTCGGCGCATGTTGGCTTCTTCGACGTTGGTGCACGTCGAGTCGCTGTTTC 69
 Qy 61 CTTTGGGCGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 Db 70 CTTTGGGCGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 129
 Qy 121 AAATTGCTATGCTAGAAATACACTCCCTTCAAATGTCCTGCTGCTGCTGCTGCTGCTGCT 180
 Db 130 AAATTGCTATGCTAGAAATACACTCCCTTCAAATGTCCTGCTGCTGCTGCTGCTGCTGCT 189
 Qy 181 GACGTCGTGTCAGAACTGTTTGCAGGTACATTTGTCAGGCGCCCTGCGGAAATCCCC 240
 Db 190 GACGTCGTGTCAGAACTGTTTGCAGGTACATTTGTCAGGCGCCCTGCGGAAATCCCC 249
 Qy 241 CATACTCAAGACAAATGTGAAGTGTCCACCGAGAACTTTCACAGAGAAAGATAATTAC 300
 Db 250 CATACTCAAGACAAATGTGAAGTGTCCACCGAGAACTTTCACAGAGAAAGATAATTAC 309
 Qy 301 CTGGATGCTTGATATCTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGC 360
 Db 310 CTGGATGCTTGATATCTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGC 369
 Qy 361 TCAGCCACAGTACCGGAAATGCGAGTCCGGAACAGCTCTTTACTACTATGACCCAAA 420
 Db 370 TCAGCCACAGTACCGGAAATGCGAGTCCGGAACAGCTCTTTACTACTATGACCCAAA 429
 Qy 421 TTTCCAGAACTGTCGCGCCCATGTACCAAGTGTCCCAAGAACTCCCTGCTCCACGAA 480
 Db 430 TTTCCAGAACTGTCGCGCCCATGTACCAAGTGTCCCAAGAACTCCCTGCTCCACGAA 489
 Qy 481 TGCAACTCCACAGCTAACTGTGTGAGTTTCATCTGTTTCAAATCCCAAGAAACCGGCTG 540
 Db 490 TGCAACTCCACAGCTAACTGTGTGAGTTTCATCTGTTTCAAATCCCAAGAAACCGGCTG 549
 Qy 541 TTCTACTGTTATCACCTTTGAGTGTGCTAATGTGTGCTGCTGCTGCTGCTGCTGCTGCT 600
 Db 550 TTCTACTGTTATCACCTTTGAGTGTGCTAATGTGTGCTGCTGCTGCTGCTGCTGCTGCT 609
 Qy 601 AGAAGATAAAGGTTCTACAGATGTTTCTTAGCTTCCTTTTATTGCTATGAAGTGATACT 660

Db 610 AGAAGATAAAGGTTCTACAGATGTTTCTTAGCTTCCTTTTATTGCTATGAAGTGATACT 669
 Qy 661 ATGAGGCAAACTCTTTTATTATTTTATTATTTTATTATTTTAAATCTCTTGAACCTTGAT 720
 Db 670 ATGAGGCAAACTCTTTTATTATTTTATTATTTTATTATTTTAAATCTCTTGAACCTTGAT 729
 Qy 721 TTGAAGACCAAGGCTGGCTCAAAATCAAGAGATCCAGACTAAGACAACTCTAATAAGGG 780
 Db 730 TTGAAGACCAAGGCTGGCTCAAAATCAAGAGATCCAGACTAAGACAACTCTAATAAGGG 789
 Qy 781 AAACATTAAATGGGACTGCTTACAGTTTTCGACGCTTTTGTCCATGATTTATCATAGTGG 840
 Db 790 AAACATTAAATGGGACTGCTTACAGTTTTCGACGCTTTTGTCCATGATTTATCATAGTGG 849
 Qy 841 GAAGCATGGCAGCATCTAAGCAGACATGATGTTTGGAGAAGGAGCTGAGATTTCTGCATCT 900
 Db 850 GAAGCATGGCAGCATCTAAGCAGACATGATGTTTGGAGAAGGAGCTGAGATTTCTGCATCT 909
 Qy 901 TGATCTGCAAGCAATAAAGGAGACTGTGTGCCACACTATACACAGCTTGAACATAGGAG 960
 Db 910 TGATCTGCAAGCAATAAAGGAGACTGTGTGCCACACTATACACAGCTTGAACATAGGAG 969
 Qy 961 ACCTCAAAGCCTGTGCCACAGTGACAAATCTTCTCCAAACAAAGGTCACTCTCTAATAA 1020
 Db 970 ACCTCAAAGCCTGTGCCACAGTGACAAATCTTCTCCAAACAAAGGTCACTCTCTAATAA 1029
 Qy 1021 TACCATTCTTATGAGCAAGCATTTCAAACACATGAGTCTATGAGGGCCAAACCAATTC 1080
 Db 1030 TACCATTCTTATGAGCAAGCATTTCAAACACATGAGTCTATGAGGGCCAAACCAATTC 1087
 Qy 1081 AACACACAGAGTTAAACAATGGCTCTGACGCTCTCTGTGGAGGCGCTCTCTTGAGAGT 1140
 Db 1088 AACACACAGAGTTAAACAATGGCTCTGACGCTCTCTGTGGAGGCGCTCTCTTGAGAGT 1147
 Qy 1141 AAGTAAACAATTTAGATGAAGGCAAGTCTCGGTATCAGGTCCAAAGAACTCAGAGATGAA 1200
 Db 1148 AAGTAAACAATTTAGATGAAGGCAAGTCTCGGTATCAGGTCCAAAGAACTCAGAGATGAA 1207
 Qy 1201 TGFTCCACTGTGGTTCCTATTAAACATACTAAGAACATGACCTCACTTACAGCTTCCA 1260
 Db 1208 TGFTCCACTGTGGTTCCTATTAAACATACTAAGAACATGACCTCACTTACAGCTTCCA 1267
 Qy 1261 CCTCACTGACTTCCCTTCCCTAGCTTCTATTCAGGTAACCCCTGCCATTTTTCGTA 1320
 Db 1268 CCTCACTGACTTCCCTTCCCTAGCTTCTATTCAGGTAACCCCTGCCATTTTTCGTA 1327
 Qy 1321 ATGTGCTTCTTGTGTTCTTCTCTCTTCCCTCTCTTCTGCTCTTCTTCTTCTTCTTCT 1380
 Db 1328 ATGTGCTTCTTGTGTTCTTCTCTCTTCCCTCTCTTCTGCTCTTCTTCTTCTTCTTCT 1387
 Qy 1381 TCTCCCACTCTCCACAGCTCTCTTTAAGGCTGAATCAGTCTGTAGGTCATGTTTAAT 1440
 Db 1388 TCTCCCACTCTCCACAGCTCTCTTTAAGGCTGAATCAGTCTGTAGGTCATGTTTAAT 1447
 Qy 1441 CTACTACTTCTCTGCTCTGAGCTCATCAGATGCTCTGCTGCTGAGCTCTCCCTCCTA 1500
 Db 1448 CTACTACTTCTCTGCTCTGAGCTCATCAGATGCTCTGCTGCTGAGCTCTCCCTCCTA 1507
 Qy 1501 TCTACATAAAGCCCTTCCCTTAAACCAAGAAATGCAAAA 1539
 Db 1508 TCTACATAAAGCCCTTCCCTTAAACCAAGAAATGCAAAA 1546

RESULT 2

AK012838

LOCUS

DEFINITION

AK012838 2276 bp mRNA linear HTC 03-APR-2004
 Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
 enriched library, clone:2810028K06 product:Tumor necrosis factor
 receptor superfamily member 21, full insert sequence.

ACCESSION

AK012838

VERSION

AK012838.1

KEYWORDS

HTC; CAP trapper.

through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence 5' GAGAGAGAGATTCCTCGAGTTAAATTAATCCCCCCCCCCC 3'. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.

Host: SOLR.

Location/Qualifiers

1..2276

/organism="Mus musculus"

/mol_type="mrna"

/strain="C57BL/6J"

/db_xref="PANTOM DB:2810028K06"

/db_xref="taxon:10090"

/clone="2810028K06"

/tissue_type="whole body"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="10, 11 days embryo"

126..551

/note="unnamed protein product; Tumor necrosis factor receptor superfamily member 21 putative"

/codon_start=1

/protein_id="BAB28502.2"

/db_xref="GI:26377809"

/translation="MLELHSPKCPAGEYMSKDVCKNCSAGTFVKAPCEIPHTGOCCEKCHPTFKQNYLDICSLCSTCDKQEWVADCSATSDRKQCRKGLYYIDPKPPESSRPCTCKPQIPLVQECNSTANTVCSSSVRRSSASVAMPI"

ch 95.2%; Score 1475.8; DB 3; Length 2276;

1 Similarity 97.0%; Pred. No. 0;

332; Conservative 0; Mismatches 2; Indels 45; Gaps 1

6 CTCGGCCATGTTGGCTTCTCTGCAGCTGGTGTCCAGTCTGAGTCGCTGGTTCCTTTG 65

2 CTCGGCCATGTTGGCTTCTCTGCAGCTGGTGTCCAGTCTGAGTCGCTGGTTCCTTTG 61

66 GCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAATAATT 125

62 GCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAATAATT 121

26 TGCTATGCTAGAAATACACTCCTTCAAATGTCCGCTGGTGAATCTGGTCTAAAGACGT 185

22 TGCTATGCTAGAAATACACTCCTTCAAATGTCCGCTGGTGAATCTGGTCTAAAGACGT 181

86 CTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGCGCCCTGCAGAAATCCCCATAC 245

82 CTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGCGCCCTGCAGAAATCCCCATAC 241

46 TCAAGGACAATGTGAGAAAGTGTCAACCAGAAACATTCACAGAGAAAGATAATTACTGGA 305

42 TCAAGGACAATGTGAGAAAGTGTCAACCAGAAACATTCACAGAGAAAGATAATTACTGGA 301

06 TGCTTTGATACCTTTGCTCCACCTGTGATAAGATCAGGAATGTCGCCGACTGCTCAGC 365

02 TGCTTTGATACCTTTGCTCCACCTGTGATAAGATCAGGAATGTCGCCGACTGCTCAGC 361

66 CACCACTGACCGGAAATGCCAGTCCGGAACAGGTCCTTTACTCTATGACCCAAAATTTCC 425

62 CACCACTGACCGGAAATGCCAGTCCGGAACAGGTCCTTTACTCTATGACCCAAAATTTCC 421

26 AGAATCGTCCGCCCAATGATCAAGTGTCCCAAGGAATCCCTGCTCTCAGGAATGCAA 485

22 AGAATCGTCCGCCCAATGATCAAGTGTCCCAAGGAATCCCTGCTCTCAGGAATGCAA 481

86 CTCCACAGCTAACACATGTGTGCGAGTTTCATCTGTTTCAA----- 523

82 CTCCACAGCTAACACATGTGTGCGAGTTTCATCTGTTTCAAAGGAAGATCTGCCTCAGTGGCCTG 541

24 -----ATCCAGAAACCGGCTGTTTCTACTGTTTATCACCTTT 560

42 GCCTATCTGAATGGTTCCAGAGATCCAGAAACCGGCTGTTTCTACTGTTTATCACCTTT 601

FEATURES	source
CDS	
ORIGIN	
Query Match	
Best Local	
Matches 1	
QY	1
Db	1
QY	1
Db	1
QY	1
Db	1
QY	2
Db	2
QY	3
Db	3
QY	3
Db	3
QY	4
Db	4
QY	4
Db	4
QY	5
Db	5

Qy	561	GAGTGTGCTAAATTGTGTCGCGTTGTGTCTCCCGTATCATAAAGAATAAAGGTTCTACAG	620
Db	602	GAGTGTGCTAAATTGTGTCGCGTTGTGTCTCCCGTATCATAAAGAATAAAGGTTCTACAG	661
Qy	621	ATGTTTTTCTTAGCTTCCTTTTATTTGCTATGAAGTGATCTATGAGGCAACTCTTTTATT	680
Db	662	ATGTTTTTCTTAGCTTCCTTTTATTTGCTATGAAGTGATCTATGAGGCAACTCTTTTATT	721
Qy	681	TTATTTATTTTATTTATTTTATTTTAAATGCTCTTGAACTTTGATTTGAAGACCCAGGCTGGCCTC	740
Db	722	TTATTTATTTTATTTATTTTATTTTAAATGCTCTTGAACTTTGATTTGAAGACCCAGGCTGGCCTC	781
Qy	741	AAAATCACAGAGATCCAGACTAAGACAACTCTAATAAGGGGAAACATTTAATTTGGACTGG	800
Db	782	AAAATCACAGAGATCCAGACTAAGACAACTCTAATAAGGGGAAACATTTAATTTGGACTGG	841
Qy	801	CTTACAGTTTTCGGAGCTTTTGTCCATGATATCATAGTGGGAAGCATGGCAGCATCTAAG	860
Db	842	CTTACAGTTTTCGGAGCTTTTGTCCATGATATCATAGTGGGAAGCATGGCAGCATCTAAG	901
Qy	861	CAGACATGATGTTTGGAGAAGGAGCTGAGATTTCTGCACTCTTGATCTCTCAAGCAATAAAG	920
Db	902	CAGACATGATGTTTGGAGAAGGAGCTGAGATTTCTGCACTCTTGATCTCTCAAGCAATAAAG	961
Qy	921	GAGACTGTGTCACACATATACACAGCTTGAAACATAGGAGACCTCAAGAGCTGTCCCCAC	980
Db	962	GAGACTGTGTCACACATATACACAGCTTGAAACATAGGAGACCTCAAGAGCTGTCCCCAC	1021
Qy	981	AGTGACAAACTTCTCTCCAAAGGTCATACCTCTCTAATAATACCATTTCTTATGAGGCAA	1040
Db	1022	AGTGACAAACTTCTCTCCAAAGGTCATACCTCTCTAATAATACCATTTCTTATGAGGCAA	1081
Qy	1041	GCATTTCAAAACACATGAGTCTATGAGGGCCAAACCAATTTCAAAACCAACAGGTTAACAAT	1100
Db	1082	GCATTTCAAAACACATGAGTCTATGAGGGCCAAACCAATTTCAAAACCAACAGGTTAACAAT	1141
Qy	1101	TGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCTTGAGAGTAAGTAAACAAATTTAGATGAAG	1160
Db	1142	TGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCTTGAGAGTAAGTAAACAAATTTAGATGAAG	1201
Qy	1161	GCAAGTCTCTGGTATCAGGTCCTCAAAAGAAACTCAGGATGAATGGTTCCTAT	1220
Db	1202	GCAAGTCTCTGGTATCAGGTCCTCAAAAGAAACTCAGGATGAATGGTTCCTAT	1261
Qy	1221	TAACATATGAGAAACATGACCTCACCTTACAGCTCTCCACCTCAGCTTCCCTTCCC	1280
Db	1262	TAACATATGAGAAACATGACCTCACCTTACAGCTCTCCACCTCAGCTTCCCTTCCC	1321
Qy	1281	CTAGCTTCTCAATTTCCAGGTAACCTGCATTTTTTGGTAATGTCCTTTGGTTCCTC	1340
Db	1322	CTAGCTTCTCAATTTCCAGGTAACCTGCATTTTTTGGTAATGTCCTTTGGTTCCTC	1381
Qy	1341	CTCTCTTTTCCCCTCTCTTCTGGTCCCTTACTTCTTCTCTCCCTCTCCACCGCC	1400
Db	1382	CTCTCTTTTCCCCTCTCTTCTGGTCCCTTACTTCTTCTCTCCCTCTCCACCGCC	1441
Qy	1401	TCCTCTTAAAGCCCTGAATCAGTCTGTAGGTCATGTTTAACTACTACTTCTCTCTGCTC	1460
Db	1442	TCCTCTTAAAGCCCTGAATCAGTCTGTAGGTCATGTTTAACTACTACTTCTCTCTGCTC	1501
Qy	1461	TGGACTCATTCAGATGTCCTCTGGGCTGAGCTCTCCCTCTCTACTACTACTACTCTCTGCTC	1520
Db	1502	TGGACTCATTCAGATGTCCTCTGGGCTGAGCTCTCCCTCTCTACTACTACTACTCTCTGCTC	1561
Qy	1521	CCTTAACAGAAATGCAAAA	1539
Db	1562	CCTTAACAGAAATGCAACA	1580

RESULT 3

BY711952

LOCUS

DEFINITION

Accession	Length	Library	EST
BY711952	1003 bp	mRNA	linear
BY711952	full-length enriched	10, 11 days embryo	whole body
DN			

ACCESSION	Mus musculus cDNA clone 2810028K06 5', mRNA sequence.
VERSION	BY711952
KEYWORDS	BY711952.1 GI:27123215
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 1003)
REFERENCE	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Xysobach, C., Gojobori, T., Baidarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusici, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Glessi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Nunata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanaigisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	22354683
PMID	12466851
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Sueno-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuchi, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Query Match	48:5†	Score 752.4;	DB 7;	Length 756;
Best Local Similarity	99.6†	Pred. No. 5.6e-175†		
Matches 753;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	556	CCCTTTGAGTGTGCTAAATTTGTCGCGTTGTTGTCTTCCTCGGTATCATTAAGAAGATAAAGGTTTC	615	
pb	1	CCCTTTGAGTGTGCTAAATTTGTCGCGTTGTTGTCTTCCTCGGTATCATTAAGAAGATAAAGGTTTC	60	


```

KEYWORDS      EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      1 (bases 1 to 708)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cga@bbs-remail.nih.gov
                Tissue Procurement: Dr. Jim Lin, University of Iowa
                cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
                cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                Clone Distribution: Distribution information can be found at
                http://genome.uiowa.edu/distribution/mousefl.html
                This clone was contributed by the Brain Molecular Anatomy Project
                (BMAP)
                The following repetitive elements were found in this cDNA
                sequence: 35-71, >(CAG)n#simple_repeat (matched complement)
                643-670, >(TAAAA)n#simple_repeat (matched complement)
                Seq primer: pyX-5.

FEATURES      Location/Qualifiers
             1..708
             /organism="Mus musculus"
             /mol_type="mRNA"
             /strain="C57BL/6"
             /db_xref="taxon:10090"
             /clone="IMAGE:6848608"
             /tissue_type="whole brain"
             /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
             /lab_host="DH10B (T1 phage resistant)"
             /clone_lib="NIH_BMAP_FY0"
             /note="Organ: Brain; Vector: pyX- Asc; Site 1: EcoR I;
             Site 2: Not I; The library was constructed according
             Bonaïdo, Lennon and Soares, Genome Research, 6:791-806,
             1996. Denatured RNA was size fractionated on a 1% agarose
             gel. First strand cDNA synthesis was primed with oligo-dT
             primer containing a Not I site. Double strand cDNA was
             size selected according to mRNA size fraction, ligated
             with EcoR I adaptor, digested with NotI and then cloned
             directionally into pyX-Asc vector. The library tag
             sequence located between the Not I site and the polyA tail
             is AGCAGACAG. This library was created for the University
             Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
             Developing Mouse Nervous System', supported by National
             Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
             program coordinator."

ORIGIN
Query Match      45.7%; Score 708; DB 6; Length 708;
Best Local Similarity 100.0%; Pred. No. 5.4e-164;
Matches 708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32  GCTTGGTGCAGTCTGAGTGGCTGCTTTCCTTTGGCGCGGCTGCTGCTGCTGCTGTC 91
Db 1  GCTTGGTGCAGTCTGAGTGGCTGCTTTCCTTTGGCGCGGCTGCTGCTGCTGCTGTC 60
Qy 92  TGCTGCTGCTCAATCTGCGCCCTTGCGAGGTAAATTTGCTATGCTAGAAATTACACTCCTTCA 151
Db 61  TGCTGCTGCTGAATCTGCGCCCTTGCGAGGTAAATTTGCTATGCTAGAAATTACACTCCTTCA 120
Qy 152  AATGTCCCGCTGGTGAATCTAGTCTAAAGACGCTGTGTTGCAAGAACTGTTCTCAGGTA 211
Db 121  AATGTCCCGCTGGTGAATCTAGTCTAAAGACGCTGTGTTGCAAGAACTGTTCTCAGGTA 180
Qy 212  CATTGTCAAGCGCCCTGCGAAATCCCCATACCTCAAGGCATGTGAGAGTGTCA 271
Db 181  CATTGTCAAGCGCCCTGCGAAATCCCCATACCTCAAGGCATGTGAGAGTGTCA 240
Qy 272  CAGGAACATTTCACAGAGAAAGATAATTACCTGGATGCTTGTATATCTTGTCTCCACCTGTG 331

```

```

Db 241  CAGGAACATTTCACAGAGAAAGATAATTACCTGGATGCTTGTATATCTTGTCTCCACCTGTG 300
Qy 332  ATAAAGATCAGGAAATGGTGGCGGACGTGCTCAGCCACCACTGAGCGGAAATGCCAGTGCC 391
Db 301  ATAAAGATCAGGAAATGGTGGCGGACGTGCTCAGCCACCACTGAGCGGAAATGCCAGTGCC 360
Qy 392  GACACAGTCTTTACTACTATGACCCCAAAATTTCCAGAAATCGTCCGCCCACTGTACCAAGT 451
Db 361  GACACAGTCTTTACTACTATGACCCCAAAATTTCCAGAAATCGTCCGCCCACTGTACCAAGT 420
Qy 452  GTCCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACAGCTAAACACTGTGTGCAGTT 511
Db 421  GTCCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACAGCTAAACACTGTGTGCAGTT 480
Qy 512  CATCTGTTTCAATCCAGAAACCGGCTGTCTCTTCTGTTATCATCCTTGGAGTGTCTAA 571
Db 481  CATCTGTTTCAATCCAGAAACCGGCTGTCTCTTCTGTTATCATCCTTGGAGTGTCTAA 540
Qy 572  TTGTGTCGGTGTGTCTTCGGTATCATAGAGATAAAGTTCTACAGATGTTTCTTA 631
Db 541  TTGTGTCGGTGTGTCTTCGGTATCATAGAGATAAAGTTCTACAGATGTTTCTTA 600
Qy 632  GCTTCCCTTTTATGCTATGAAGTGATCTATGAGGCAACTCTTTTATTTATTTATTTT 691
Db 601  GCTTCCCTTTTATGCTATGAAGTGATCTATGAGGCAACTCTTTTATTTATTTATTTT 660
Qy 692  ATTTTATTTTATGCTTGAAGTGTGAACTTGAATTTGAAGACACCGCTGGCCT 739
Db 661  ATTTTATTTTATGCTTGAAGTGTGAACTTGAATTTGAAGACACCGCTGGCCT 708

RESULT 8
BU611594
LOCUS       BU611594               696 bp      mRNA      linear      EST 20-FEB-2003
DEFINITION UT-M-F10-cav-h-06-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA clone
ACCESSION  BU611594
VERSION    BU611594.1 GI:23277809
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE   1 (bases 1 to 696)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cga@bbs-remail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            The following repetitive elements were found in this cDNA
            sequence: 39-75, >(CAG)n#simple_repeat (matched complement)
            647-674, >(TAAAA)n#simple_repeat (matched complement)
            Seq primer: pyX-5.

FEATURES      Location/Qualifiers
             1..696
             /organism="Mus musculus"
             /mol_type="mRNA"
             /strain="C57BL/6"
             /db_xref="taxon:10090"
             /clone="UI-M-F10-cav-h-06-0-UI"
             /tissue_type="whole brain"
             /dev_stage="embryo 12.5dpc"
             /lab_host="DH10B (T1 phage resistant)"
             /clone_lib="NIH_BMAP_F10"
             /note="Organ: Brain; Vector: pyX- Asc; Site 1: EcoR I;

```



```

QY 292 GATATTAACCTGGATGCTTGTATATCTTGTCCACCTGTGATGAAGATCAGGAATGCTG 351
Db 241 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 352 GCCGACTGCTCAGCCACAGTGCACGGGAAATGCCAGTCCCGAAGAGTCTTTACTACTAT 411
Db 300 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 412 GACCCAAATTCGAAATCGTGGCGGCCATGTACCAAGTGTCCCAAGGAATCCCTGTC 471
Db 360 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 472 CTCGAGGAATGCACTCCACAGCTAACACTGTGTGAGTGTCTATCTGTTTCAATCCCGA 531
Db 420 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 532 AACCGGCTGTTCTTACTGTTTATCACTTTGAGTGTGCTAAATGTGTCGGTTGTTGCTTC 591
Db 480 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 592 CGTATCATAAGAAAGTTCACAGATGTTTCTTACGCTTCTTTATGCTATGA 651
Db 540 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 652 AGTGATCTATGGAGGCACTCTTTATTTATTTATTTATTTATTTATTTATTTATTTAT 711
Db 600 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 712 GAACCTTGATTTGAAGACCAAGGCTG 735
Db 660 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 10
AW544660/c
LOCUS C0184C12-3 NIA Mouse E7.5 Extraembryonic Portion cDNA Library Mus
DEFINITION musculus cDNA clone C0184C12 3', mRNA sequence.
ACCESSION AW544660
VERSION AW544660.1 GI:7187077
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 552)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,
Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
20381348
10922068
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: C0184 row: C column: 12
Seg primer: -21M13 Forward
High quality sequence stop: 552
POLYA=yes.
Location/Qualifiers
1..552
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:C0184C12-3"
/db_xref="taxon:10090"
/clone="C0184C12"
/sex="unknown"
/dev_stage="7.5dpc Embryo"
FEATURES
source

```

```

/lab_host="DH10B"
/clone_lib="NIA Mouse E7.5 Extraembryonic Portion cDNA
Library"
/note="vector: pSPORT1 (Gibco/BRL Life Technology);
Site 1: SalI; Site 2: NotI; Total RNAs were extracted from
5 EPC. The double-stranded cDNA was synthesized by
Gibco's kit with an Oligo(dT) primer [NotI primer-adaptor
from GibcoBRL]
[5'-pGACTAGTCTTAGATCGAGGCGCGCCCTTTTCTTTTCTTTT-3']
from 0.8ug of mRNA. The double-stranded cDNAs were
treated with T4 DNA polymerase and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker L1-Sal3 (include SalI sequence). The cDNAs
were purified by phenol/chloroform and separated from
free linkers by Centricon 100. Then, cDNAs were amplified
by long-range high fidelity PCR using Takara's Ex Taq
polymerase. Then, the cDNAs were purified by
phenol/chloroform and by Centricon 100. The cDNAs were
digested with SalI and NotI enzymes. Then, the cDNAs were
size selected by Gibco's Size Fractionation Column. The
cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by chemical method. The library was
constructed by Xiaohong Wang."

```

ORIGIN

```

Query Match 34.8%; Score 539.2; DB 2; Length 552;
Best Local Similarity 98.6%; Pred. No. 3.1e-122;
Matches 544; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 978 CACAGTCACAACTTCCTCCAAACAGGTCTACCTCTTAATATACCAATTTCTTTATGAGG 1037
Db 552 CACAGTCACAACTTCCTCCAAACAGGTCTACCTCTTAATATACCAATTTCTTTATGAGG 493
QY 1038 CAAGCATTTCAAAACATGAGTCTATGAGGGCCAAACCAATTTCAAAACCAACACAGGTTAAC 1097
Db 492 CAAGCATTTCAAAACATGAGTCTATGAGGGCCAAACCAATTTCAAAACCAACACAGGTTAAC 433
QY 1098 AATTGCCCTCTGAGCTCTCTGTGGAGGGCCCTCTTGGAGAGTAAGTAACAAATTTAGATG 1157
Db 432 AATTGCCCTCTGAGCTCTCTGTGGAGGGCCCTCTTGGAGAGTAAGTAACAAATTTAGATG 373
QY 1158 AAGCAAGTCTGTGTATCAGGTCCAAAGAAACTCAGATGCAATGGTCCACTGTGGTTCC 1217
Db 372 AAGCAAGTCTGTGTATCAGGTCCAAAGAAACTCAGATGCAATGGTCCACTGTGGTTCC 313
QY 1218 TATTAACATATCTGAAGAACATGACCTCACCTTACACGTCCTCCACCTCACTGACATTCCTT 1277
Db 312 TATTAACATATCTGAAGAACATGACCTCACCTTACACGTCCTCCACCTCACTGACATTCCTT 253
QY 1278 CCCCTAGCTTCTCAATCCAGGTAAACCTGCCATTTTGTGTATGTGCTTCTTGGTTC 1337
Db 252 CCCCTAGCTTCTCAATCCAGGTAAACCTGCCATTTTGTGTATGTGCTTCTTGGTTC 193
QY 1338 TTCTCTCTCTTCCCTCTCTCTGTGTCTTACTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1397
Db 192 TTCTCTCTCTTCCCTCTCTCTGTGTCTTATTTCTTCTCTCTCTCTCTCTCTCTCTCTCT 133
QY 1398 GCCTCTCTTTAAGCCCTGAATCAGTCTGTAGGTCAATGTTTAATCTACTATTTCTCTCTG 1457
Db 132 GCCTCTCTTTAAGCCCTGAGTCTGAGTCTGAGGCCATGTTTAATCTACTATTTCTCTCTG 73
QY 1458 CTCTGGACTCATCCAGATGCTCTGTGGCTGAGCTCTCCCTCTCTATCTCAATTAACCCCTT 1517
Db 72 CTCTGGACTCATCCAGATGCTCTGTGGCTGAGCTCTCCCTCTCTATCTATCTATCAATAAACCCCTT 13
QY 1518 CCCCCTAACACAG 1529
Db 12 CCCCCTAACACAG 1

```

RESULT 11
CB587413

LOCUS CB587413 863 bp mRNA linear EST 03-APR-2003
 DEFINITION AGNCOURT_12970406 NIH MGC_136 Mus musculus cDNA clone
 IMAGE:30294625 5', mRNA sequence.
 ACCESSION CB587413
 VERSION CB587413.1 GI:29505269
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. David Rowe
 CDNA Library Preparation: Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: NDAM342 row: a column: 02
 High quality sequence stop: 550.
 FEATURES
 Location/Qualifiers
 1..863
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:30294625"
 /tissue_type="embryonic limb, maxilla and mandible"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 136"
 /note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Normalized, full-length enriched library from pool of mouse embryonic limb, maxilla and mandible, embryonic day 17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw equivalents from respective days). Cloned directionally, oligo-dr primed (5'-GACTAGTCTAGATCGCGCGCCGCTT)15-3'. Size selected for the 1kb fragments, average insert size 1.2 kb. Normalization to Cot 7.5. Tissue contributed by David Rowe; library constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
 ORIGIN
 Query Match 32.6%; Score 505.4; DB 6; Length 863;
 Best Local Similarity 97.9%; Pred. No. 7.8e-114;
 Matches 512; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 1028 TCTTATGAGGCAAGCATTCAACACATGAGTCTATGAGGCGCAACCAATTCAAACACC 1087
 Db 1 TCTTATGAGGCAAGCATTCAACACATGAGTCTATGAGGCGCAACCAATTCAAACACC 60
 1088 ACAGTTTAACTTGCCTCTGAGCTCTCTGTTGAGGCGCCCTCTTGTAGATGATTAAC 1147
 Db 61 ACAGTTTAACTTGCCTCTGAGCTCTCTGTTGAGGCGCCCTCTTGTAGATGATTAAC 120
 1148 AATTAGATGAGCAAGTCTCTGTATCAGTCTCAAGAAAGAACTCAGATGATGTGCA 1207
 Db 121 AATTAGATGAGCAAGTCTCTGTATCAGTCTCAAGAAAGAACTCAGATGATGTGCA 180
 1208 CTGTGGTTCCTATTAACTACTGAAGAACATGACCTCACCTTACACGCTCTCCACCTCACT 1267
 Db 181 CTGTGGTTCCTATTAACTACTGAAGAACATGACCTCACCTTAGACTTCTCCACCTCACT 240
 1268 GACTTCCCTTCCCTAGCTTCTCATTTCCAGGTAACCTTGCCTATTTTGGTATGTGCC 1327
 Db 241 GGCTTCCCTTCCCTAGCTTCTCATTTCCAGGTAACCTTGCCTATTTTGGTATGTGCC 300
 1328 TTCTTGGTTCCTCTCTCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1387
 Db 301 TTCTTGGTTCCTCTCTCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360

Qy 1388 CTCTCACACGAGCTCTCTTAAAGGCTGAATCAGTCTGTAGGTCATGTTTAACTACTAC 1447
 Db 361 CTCTCCACACGAGCTCTTAAAGGCTGAATCAGTCTGTAGGCTGAGTCTGAGGCGCCATGTTTAACTACTAC 420
 Qy 1448 TTTCTCTCTGCTCTGGACTCATCCAGATGCTCTGGCTGAGCTCTCCCTCTATCTACAA 1507
 Db 421 TTTCTCTCTGCTCTGGACTCATCCAGATGCTCTGGCTGAGCTCTCCCTCTATCTACAA 480
 Qy 1508 TAAACCCCTTCCCTTAACACAGAAATGCRAAAAAAAAAAAAAA 1550
 Db 481 TAAACCCCTTCCCTTAACACAGAAATGCRAAAAAAAAAAAAAA 523
 RESULT 12
 BI788944
 LOCUS ie4le08.y1 Kaestner ngn3 wt Mus musculus cDNA 5', mRNA sequence.
 DEFINITION BI788944
 ACCESSION BI788944.1 GI:15816669
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 480)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Mavris, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000) Library was constructed by Catherine Lee DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Marie Searce (msearce@mail.med.upenn.edu)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 429.
 Location/Qualifiers
 1..480
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129/Sv x CD1"
 /db_xref="taxon:10090"
 /dev_stage="p.c. 14.5"
 /lab_host="E. coli-DH12S (GIBCO)"
 /clone_lib="Kaestner ngn3 wt"
 /note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_1: Not I; Site_2: Sal I; The library was prepared by Catherine S. Lee and has not been published. The pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000). The cDNA's were prepared with an oligo containing a NotI site, and SalI linkers were added to the ends. The inserts were cut with NotI before being cloned into the NotI-SalI sites in the vectors. This is one of two libraries, ngn3 wt and ngn3 -/- . The wt library is in pSPORT1, T7 promoter is 5'."
 FEATURES
 source
 Query Match 29.7%; Score 460.4; DB 4; Length 480;
 Best Local Similarity 99.8%; Pred. No. 9.5e-103;
 Matches 461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 ORIGIN

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgsbbs-remail.nih.gov
Tissue Procurement: Dr. Minoru Ko, Dr. Janet Rossett, Dr. Janet Rossett
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 18-305, >RMR10A#LTR (matched complement)
Seq primer: M13 FORWARD
PolyA=yes.

FEATURES
source

Location/Qualifiers
1..458
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/tissue_type="Trophoblast"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP PlTr1"
/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI CGAP PlTr1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are GGTGG, ATCAT, GGGTG, GGTGG. For additional information, contact: Bento Soares, bento-soares@uiowa.edu
TAG_TISSUE=placenta mouse 11.5-12.5 days
TAG_LIB=UI-1-CFO
TAG_SEQ=ATCAT"

ORIGIN

Query Match 28.3%; Score 438.8; DB 5; Length 458;
Best Local Similarity 97.4%; Pred. No. 2.1e-97;
Matches 446; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1088 ACAGGTTAAACAATTGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCTTTGAGAGTAAGTAAC 1147
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 458 ACAGGTTAAACAATTGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCTTTGAGAGTAAGTAAC 399
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1148 AATTTAGATGAAGCAAGTCTCTGTATCAGGTCCAAAGAAACTCAGGATGAATGGTCCA 1207
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 398 AATTTAGATGAAGCAAGTCTCTGTATCAGGTCCAAAGAAACTCAGGATGAATGGTCCA 339
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1208 CTGTGGTTCCTATTAAACATCTGAACATGACCTCACCTTACACCTCTCCACCTCACT 1267
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 338 CTGTGGTTCCTATTAAACATCTGAACATGACCTCACCTTACACCTCTCCACCTCACT 279
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1268 GACTTCCCTTCCCTTAGCTTCTCATTCAGGTAAACCTGCATTTTGGTAAATGTGCC 1327
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 278 GGCTTCCCTTCCCTTAGCTTCTCATTCAGGTAAACCTGCATTTTGGTAAATGTGCC 219
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1328 TTCTTGGTTCCT 1387
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 218 TTCTTGGTTCCT 159
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1388 CTCTCCACCAAGCT 1447
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 158 CTCTCCACCAAGCT 99
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1448 TTCT 1507
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 98 TTTCTCTCTGCTTGGACTCATCCAGATGTCTCTGGCTGAGCTCTCCCTCTCTATACAA 39
Qy 1508 TAAACACCTTTCCCTTAACCCAGAAATGCAAAAAA 1545
Db 38 TAAACACCTTTCCCTTAACCCAGAAATGCAAAAAA 1

Search completed: September 9, 2005, 06:50:08
Job time : 18117.6 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 17:05:32 ; Search time 598.714 Seconds
(without alignments)
127.905 Million cell updates/sec

Title: US-10-622-407-8
Perfect score: 1087
Sequence: 1 MFGFFCSLVSLSRFLWRR.....LLSPLSLVLSVVVFRIIRR 198

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1087	100.0	198	7	ABW02715
2	1087	100.0	198	8	ADJ45752 Murine tm
3	962	88.5	398	7	ABW02717
4	962	88.5	398	8	ADJ45758 Murine tm
5	956	87.9	180	7	ABW02716
6	956	87.9	180	8	ADJ45754
7	748	68.8	133	7	ABW02714
8	748	68.8	133	8	ADJ45750
9	746.5	68.7	176	2	AAW80254
10	746.5	68.7	176	8	ADF57551
11	746.5	68.7	176	8	ADMA6623
12	711	65.4	396	8	ADF57557
13	682.5	62.8	148	8	ADMA6624
14	542.5	49.9	380	4	ABG09344
15	467	43.0	117	8	ADF57549
16	320	29.4	204	5	ABB81467
17	226	20.8	247	8	ADF57553
18	226	20.8	454	5	AAD22289
19	226	20.8	454	8	ADT08167
20	218.5	20.1	242	8	ADF57552
21	218.5	20.1	327	2	AAAR41688
22	218.5	20.1	327	2	AAAR78611
23	218.5	20.1	327	2	AAAR2530
24	218.5	20.1	327	2	AAW86241
25	218.5	20.1	327	3	AAAB19344

26	218.5	20.1	327	8	ADL27705
27	218.5	20.1	327	8	ADMS3477
28	212.5	19.5	461	7	ADJ57927
29	212.5	19.5	461	8	ADQ76809
30	211.5	19.5	461	2	ABG74754
31	211.5	19.5	461	2	AAAR07450
32	208.5	19.2	355	2	AAAR85073
33	208.5	19.2	355	4	AAAS0524
34	208.5	19.2	355	8	ADJ96165
35	207.5	19.1	285	2	AAW33359
36	205	18.9	350	5	ABB81468
37	203.5	18.7	256	2	AAW33357
38	203.5	18.7	307	2	AAW33358
39	203.5	18.7	336	2	AAW33360
40	203.5	18.7	884	2	AAAR70109
41	202.5	18.6	658	5	AAAR49759
42	201.5	18.5	168	2	AAAR24084
43	201.5	18.5	197	6	ADA49707
44	201.5	18.5	199	2	AAAR24080
45	201.5	18.5	211	2	AAW89225

ALIGNMENTS

RESULT 1	
ABW02715	
ID	ABW02715 standard; protein; 198 AA.
XX	
AC	ABW02715;
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	Mouse tmst2-receptor protein.
XX	
KW	Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis; cachexia; autoimmune disease; inflammatory disease; chromosome mapping; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunomodulator; antiinflammatory; antiparasitic; cytostatic; mouse.
XX	
OS	Mus musculus.
XX	
PN	US6627199-B1.
XX	
PD	30-SEP-2003.
XX	
PF	07-JUL-2000; 2000US-00612033.
XX	
PR	09-JUL-1999; 99US-0143063P.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Saris C;
XX	
DR	WPI; 2003-874309/81.
DR	N-PSDB; AAD64754.
XX	
PT	New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing, treating or ameliorating diseases associated with or resulting from for abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for chromosome mapping.
XX	
PS	Claim 1; SEQ ID NO 8; Opp; English.
XX	
CC	The invention relates to transmembrane decoy-receptor (tmst2) proteins and their secreted splice variants, belonging to the tumour necrosis factor (TNF) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome

```
CC identification or mapping. The invention is useful in gene therapy. The
CC present sequence is mouse tmst2-receptor protein used in the
CC exemplification of the invention
XX
XX
SQ Sequence 198 AA;
    Query Match      100.0%; Score 1087; DB 7; Length 198;
    Best Local Similarity 100.0%; Pred. No. 1e-81;
    Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLELHSFKPCPAGEYWSKDVC 60
    Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLELHSFKPCPAGEYWSKDVC 60
    Qy 61 KNCAGTFVVKAPCEIPHTQGQCEKCHPGTFTTEKDYLDACILCSTCDKQEMVADCSATS 120
    Db 61 KNCAGTFVVKAPCEIPHTQGQCEKCHPGTFTTEKDYLDACILCSTCDKQEMVADCSATS 120
    Qy 121 DRKCQCRGTGLYYDPKFPESCRCPTCKPQGIPLVLOECNSTANTVCSVSNPNRNLFLLL 180
    Db 121 DRKCQCRGTGLYYDPKFPESCRCPTCKPQGIPLVLOECNSTANTVCSVSNPNRNLFLLL 180
    Qy 181 SPLSVLIIVSVVVFRIIR 198
    Db 181 SPLSVLIIVSVVVFRIIR 198
RESULT 2
ADJ45752
ID ADJ45752 standard; protein; 198 AA.
XX
XX ADJ45752;
XX
XX 06-MAY-2004 (first entry)
XX Murine tmst2-receptor.
XX
XX Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;
XX autoimmune disease; cachexia; cancer; cerebral malaria;
XX diabetes mellitus; disseminated intravascular coagulation;
XX haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;
XX lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;
XX organ rejection; rheumatoid arthritis; septic shock; stroke;
XX adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
XX receptor.
XX
XX Mus musculus.
XX
XX US2004018544-A1.
XX
XX 29-JAN-2004.
XX
XX 17-JUL-2003; 2003US-00622407.
XX
XX 09-JUL-1999; 99US-0143063P.
XX 07-JUL-2000; 2000US-00612033.
XX
XX (SARI/) SARIS C.
XX
XX Saris C;
XX
XX WPI; 2004-224390/21.
XX N-PSDB; ADJ45751.
XX
XX Novel tmst2-receptor polypeptide useful for diagnosing and treating
XX disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
XX infections.
XX
XX Claim 13; SEQ ID NO 8; 57pp; English.
XX
XX The invention relates to a tmst2-receptor polypeptides and the
XX polynucleotide encoding them. The sequences of the invention are useful
XX for treating diseases and conditions including acquired immunodeficiency
CC
```

```
CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral
CC malaria, diabetes mellitus, disseminated intravascular coagulation,
CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,
CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ
CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory
CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.
CC This sequence represents the murine tmst2-receptor polypeptide of the
CC invention.
XX
XX
SQ Sequence 198 AA;
    Query Match      100.0%; Score 1087; DB 8; Length 198;
    Best Local Similarity 100.0%; Pred. No. 1e-81;
    Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLELHSFKPCPAGEYWSKDVC 60
    Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLELHSFKPCPAGEYWSKDVC 60
    Qy 61 KNCAGTFVVKAPCEIPHTQGQCEKCHPGTFTTEKDYLDACILCSTCDKQEMVADCSATS 120
    Db 61 KNCAGTFVVKAPCEIPHTQGQCEKCHPGTFTTEKDYLDACILCSTCDKQEMVADCSATS 120
    Qy 121 DRKCQCRGTGLYYDPKFPESCRCPTCKPQGIPLVLOECNSTANTVCSVSNPNRNLFLLL 180
    Db 121 DRKCQCRGTGLYYDPKFPESCRCPTCKPQGIPLVLOECNSTANTVCSVSNPNRNLFLLL 180
    Qy 181 SPLSVLIIVSVVVFRIIR 198
    Db 181 SPLSVLIIVSVVVFRIIR 198
RESULT 3
ABW02717
ID ABW02717 standard; protein; 398 AA.
XX
XX ABW02717;
XX
XX 11-MAR-2004 (first entry)
XX Mouse tmst2-receptor-human immunoglobulin Fc region fusion protein.
XX
XX Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
XX cachexia; autoimmune disease; inflammatory disease; chromosome mapping;
XX cancer; chromosome identification; gene therapy; antibacterial; virucide;
XX immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
XX cytostatic; mouse; human; immunoglobulin Fc region; fusion protein.
XX
XX Chimeric - Mus musculus.
XX Chimeric - Homo sapiens.
XX
XX US6627199-B1.
XX
XX 30-SEP-2003.
XX
XX 07-JUL-2000; 2000US-00612033.
XX
XX 09-JUL-1999; 99US-0143063P.
XX (AMGE-) AMGEN INC.
XX
XX Saris C;
XX
XX WPI; 2003-874309/81.
XX N-PSDB; AAD64758.
XX
XX New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,
XX treating or ameliorating diseases associated with or resulting from
XX abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
XX chromosome mapping.
XX
XX Example 4; SEQ ID NO 14; Opp; English.
XX
```

CC The invention relates to transmembrane decoy-receptor (tmst2) proteins
CC and their secreted splice variants, belonging to the tumour necrosis
CC factor (TNF) receptor super gene family and polynucleotides encoding such
CC proteins. The composition and methods are useful in diagnosing, treating
CC or ameliorating diseases associated with or resulting from abnormal tmst2
CC and/or abnormal expression of its putative ligand, such as sepsis,
CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial
CC and parasitic diseases or cancer. They may also be used for chromosome
CC identification or mapping. The invention is useful in gene therapy. The
CC present sequence is a fusion protein comprising mouse tmst2- receptor
CC protein and human immunoglobulin Fc region. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 398 AA;

Query Match 88.5%; Score 962; DB 7; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.1e-71;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGFFCSLVSSLSRWFLWRLRLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
DB 1 MFGFFCSLVSSLSRWFLWRLRLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
QY 61 KNCAGTFVKAPCEIPIHTQOQCEKCHPGTFTKXNDYLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPIHTQOQCEKCHPGTFTKXNDYLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKCQRTGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVSN 171
DB 121 DRKCQRTGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVSN 171

RESULT 4
ADJ45758
ID ADJ45758 standard; protein; 398 AA.
XX AC ADJ45758;
XX DT 06-MAY-2004 (first entry)
XX DE Murine tmst2-Fc fusion protein.
XX DE Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;
KW autoimmune disease; cachexia; cancer; cerebral malaria;
KW diabetes mellitus; disseminated intravascular coagulation;
KW haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;
KW lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;
KW organ rejection; rheumatoid arthritis; septic shock; stroke;
KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
tmst2-Fc fusion protein; receptor.
XX KW
XX OS Mus musculus.
XX OS Synthetic.
XX PN US2004018544-A1.
XX PD 29-JAN-2004.
XX PF 17-JUL-2003; 2003US-00622407.
XX PR 09-JUL-1999; 99US-0143063P.
XX PR 07-JUL-2000; 2000US-00612033.
XX PR (SARI/) SARIS C.
XX PA Saris C;
XX PI WPI; 2004-224390/21.
XX DR N-PSDB; ADJ45757.
XX DR Novel tmst2-receptor polypeptide useful for diagnosing and treating
XX disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
XX infections.
PT

XX Example 4; SEQ ID NO 14; 57pp; English.
XX The invention relates to a tmst2-receptor polypeptides and the
CC polynucleotide encoding them. The sequences of the invention are useful
CC for treating diseases and conditions including acquired immunodeficiency
CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral
CC malaria, diabetes mellitus, disseminated intravascular coagulation,
CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,
CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ
CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory
CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.
CC This sequence represents a murine tmst2-Fc fusion protein of the
CC invention.
XX
SQ Sequence 398 AA;

Query Match 88.5%; Score 962; DB 8; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.1e-71;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGFFCSLVSSLSRWFLWRLRLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
DB 1 MFGFFCSLVSSLSRWFLWRLRLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
QY 61 KNCAGTFVKAPCEIPIHTQOQCEKCHPGTFTKXNDYLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPIHTQOQCEKCHPGTFTKXNDYLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKCQRTGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVSN 171
DB 121 DRKCQRTGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVSN 171

RESULT 5
ABW02716
ID ABW02716 standard; protein; 180 AA.
XX AC ABW02716;
XX DT 11-MAR-2004 (first entry)
XX DE Mouse tmst2-receptor splice variant protein.
XX DE Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;
KW cancer; chromosome identification; gene therapy; antibacterial; virucide;
KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
KW cytostatic; mouse; splice variant.
XX KW
XX OS Mus musculus.
XX PN US6627199-B1.
XX PD 30-SEP-2003.
XX PF 07-JUL-2000; 2000US-00612033.
XX PR 09-JUL-1999; 99US-0143063P.
XX PR (AMGE-) AMGEN INC.
XX PA Saris C;
XX PI WPI; 2003-874309/81.
XX DR N-PSDB; AAD64755.
XX DR New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,
XX treating or ameliorating diseases associated with or resulting from
XX abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
XX chromosome mapping.
XX PS Claim 1; SEQ ID NO 10; 0pp; English.

XX The invention relates to transmembrane decoy-receptor (tmst2) proteins
CC and their secreted splice variants, belonging to the tumour necrosis
CC factor (TNF) receptor super gene family and polynucleotides encoding such
CC proteins. The composition and methods are useful in diagnosing, treating
CC or ameliorating diseases associated with or resulting from abnormal tmst2
CC and/or abnormal expression of its putative ligand, such as sepsis,
CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial
CC and parasitic diseases or cancer. They may also be used for chromosome
CC identification or mapping. The invention is useful in gene therapy. The
CC present sequence is mouse tmst2-receptor splice variant protein used in
CC the exemplification of the invention
XX
XX Sequence 180 AA;

Query Match 87.9%; Score 956; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.7e-71;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFGFCSLVSSLSRWFLWRLRLLLLLLLLLLPLQVRFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFCSLVSSLSRWFLWRLRLLLLLLLLLLPLQVRFAMLELHSPKCPAGEYWSKDVC 60
Qy 61 KNCAGTFVKAPCEIPHTQGCCKHPGTFTEKDYLDACILCSTCDKQEMWADCSATS 120
Db 61 KNCAGTFVKAPCEIPHTQGCCKHPGTFTEKDYLDACILCSTCDKQEMWADCSATS 120
Qy 121 DRKQCRTGLYYDPKFPESCRCCTKCPQGIPIVLECNSTANTVCSSTS 170
Db 121 DRKQCRTGLYYDPKFPESCRCCTKCPQGIPIVLECNSTANTVCSSTS 170

RESULT 6
ADJ45754
ID ADJ45754 standard; protein; 180 AA.
XX
AC ADJ45754;
XX
DT 06-MAY-2004 (first entry)
XX
DE Murine tmst2-receptor splice variant polypeptide.
XX
KW Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;
KW autoimmune disease; cachexia; cancer; cerebral malaria;
KW diabetes mellitus; disseminated intravascular coagulation;
KW haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;
KW lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;
KW organ rejection; rheumatoid arthritis; septic shock; stroke;
KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
KW tmst2-receptor splice variant; receptor.
XX
OS Mus musculus.
XX
FN US2004018544-A1.
XX
PD 29-JAN-2004.
XX
PP 17-JUL-2003; 2003US-00622407.
XX
PR 09-JUL-1999; 99US-0143063P.
PR 07-JUL-2000; 2000US-00612033.
XX
PA (SARI/) SARIS C.
XX
PI Saris C;
XX
DR WPI; 2004-224390/21.
DR N-PSDB; ADJ45753.
XX
PT Novel tmst2-receptor polypeptide useful for diagnosing and treating
PT disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
PT infections.
XX

PS Claim 13; SEQ ID NO 10; 57pp; English.
XX
CC The invention relates to a tmst2-receptor polypeptides and the
CC polynucleotide encoding them. The sequences of the invention are useful
CC for treating diseases and conditions including acquired immunodeficiency
CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral
CC malaria, diabetes mellitus, disseminated intravascular coagulation,
CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,
CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ
CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory
CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.
CC This sequence represents a murine tmst2-receptor splice variant
CC polypeptide of the invention.
XX
XX Sequence 180 AA;

Query Match 87.9%; Score 956; DB 8; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.7e-71;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFGFCSLVSSLSRWFLWRLRLLLLLLLLLLPLQVRFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFCSLVSSLSRWFLWRLRLLLLLLLLLLPLQVRFAMLELHSPKCPAGEYWSKDVC 60
Qy 61 KNCAGTFVKAPCEIPHTQGCCKHPGTFTEKDYLDACILCSTCDKQEMWADCSATS 120
Db 61 KNCAGTFVKAPCEIPHTQGCCKHPGTFTEKDYLDACILCSTCDKQEMWADCSATS 120
Qy 121 DRKQCRTGLYYDPKFPESCRCCTKCPQGIPIVLECNSTANTVCSSTS 170
Db 121 DRKQCRTGLYYDPKFPESCRCCTKCPQGIPIVLECNSTANTVCSSTS 170

RESULT 7
ABW02714
ID ABW02714 standard; protein; 133 AA.
XX
AC ABW02714;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mouse tmst2-receptor protein from tmst2-00004-d1 clone.
XX
KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;
KW cancer; chromosome identification; gene therapy; antibacterial; virucide;
KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
KW cyostatic; mouse.
XX
OS Mus musculus.
XX
FN US6627199-B1.
XX
PD 30-SEP-2003.
XX
PP 07-JUL-2000; 2000US-00612033.
XX
PR 09-JUL-1999; 99US-0143063P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Saris C;
XX
DR WPI; 2003-874309/81.
DR N-PSDB; AAD64753.
XX
PT New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,
PT treating or ameliorating diseases associated with or resulting from
PT abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
PT chromosome mapping.
XX
PS Example 1; SEQ ID NO 6; Opp; English.
XX

XX The present sequence represents a protein designated 7F4. This protein is
CC capable of inducing differentiation in osteoblast cells. The protein may
CC be used to screen compounds for the ability to bind to it, for use as
CC ligands, agonists or antagonists and inhibiting or otherwise altering its
CC differentiation inducing activity. Compounds so identified, as well as
CC the protein itself, DNA encoding it, and antibodies to it, may be used in
CC the treatment of diseases of bone growth and osteoblast differentiation,
CC such as bone sarcomas
XX
SQ Sequence 176 AA:

CC The invention relates to transmembrane decoy receptor, ymkz5 belonging to
CC tumour necrosis factor (TNF) receptor supergene family and nucleic acid
CC sequences encoding such receptors. The invention is useful for detecting
CC diseases or susceptibility to diseases related to the presence of mutated
CC ymkz5-receptor gene such as tumours or cancers. The sequences of the
CC invention are used as medication for a number of diseases such as
CC acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases,
CC cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial
CC ischaemia, obesity etc. The invention is also useful in gene therapy. The
CC present sequence is mouse ymkz5 receptor protein.
xx
xx Sequence 176 AA:
SO

Db 1 AMPESYSFNCNPDGEYQSNVDCCKTSPSGTFVKAQPKIPHTQOQCEKCHPGTFTGKNDGLH 60
 QY 99 ACILCSTCDKQEMVADCSATSDRKCQCRGTGLYYDDPKPSPSCRPCTKCPQGIPLVQECN 158
 Db 61 DCELCSTCDKQNMVADCSATSDRKCCEQIGLYYYDPKPPSPSCRPCTKCPQGIPLVQECN 120
 QY 159 STANTVCSVSNPNRFLFLLSPLSVLVSVVPR 195
 Db 121 STANTVCSVSNPNRFLFLLM-----LIVFCI 148

RESULT 14
 ABG09344
 ID ABG09344 standard; protein; 380 AA.
 AC ABG09344;
 DT 13-FEB-2002 (first entry)
 XX Novel human diagnostic protein #9335.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS
 XX WO200175067-A2.
 PN 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US008631.
 PF
 XX 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS73531.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 39703; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG030377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 380 AA;

Query Match 49.9%; Score 542.5; DB 4; Length 380;
 Best Local Similarity 80.2%; Pred. No. 1.5e-36;
 Matches 101; Conservative 0; Mismatches 0; Indels 25; Gaps 1;
 QY 8 LVSSLSRWFLWRRLLLLLLLLLLLLLPLQ-----VKFAMLE 42
 Db 47 LVSSLSRWFLWRRLLLLLLLLLLLLLPLQKAVHRKATPESAIADCSGRDCAFWVKFAMLE 106
 QY 43 LHSFKCPAGEYWSKDVCKKCSAGTFVKAPCEIPHTQOQCEKCHPGTFTKXNYLDACIL 102
 Db 107 LHSFKCPAGEYWSKDVCKKCSAGTFVKAPCEIPHTQOQCEKCHPGTFTKXNYLDACIL 166
 QY 103 CSTCDK 108
 Db 167 CSTCDK 172

RESULT 15
 ADF57549
 ID ADF57549 standard; protein; 117 AA.
 XX
 AC ADF57549;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Mouse ymkz5 receptor from clone ymkz5-00013-g11.
 XX
 KW Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour;
 KW cancer; acquired immune deficiency syndrome; AIDS; anaemia;
 KW autoimmune disease; cachexia; leprosy; leukaemia; hepatitis;
 KW multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
 KW receptor.
 XX
 OS Mus musculus.
 XX
 PN US2003096355-A1.
 XX
 PD 22-MAY-2003.
 XX
 PF 11-JUL-2002; 2002US-00193616.
 XX
 PR 09-JUL-1999; 99US-0143137P.
 PR 07-JUL-2000; 2000US-00611989.
 XX
 PA (ZHAN/) ZHANG K.
 XX
 PI Zhang K;
 XX
 DR WPI; 2004-008943/01.
 DR N-PSDB; ADF57563.
 XX
 XX Novel ymkz5-receptor polypeptide useful for treating diseases such as
 XX tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy,
 XX leukemia, hepatitis, multiple sclerosis.
 XX
 PS Example 1; SEQ ID NO 6; 57pp; English.
 XX
 CC The invention relates to transmembrane decoy receptor, ymkz5 belonging to
 CC tumour necrosis factor (TNF) receptor supergene family and nucleic acid
 CC sequences encoding such receptors. The invention is useful for detecting
 CC diseases or susceptibility to diseases related to the presence of mutated
 CC ymkz5-receptor gene such as tumours or cancers. The sequences of the
 CC invention are used as medication for a number of diseases such as
 CC acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases,
 CC cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial
 CC ischaemia, obesity etc. The invention is also useful in gene therapy. The
 CC present sequence is mouse ymkz5 receptor protein.
 XX
 XX Sequence 117 AA;

Query Match 43.0%; Score 467; DB 8; Length 117;
 Best Local Similarity 73.6%; Pred. No. 7.6e-31;
 Matches 89; Conservative 5; Mismatches 19; Indels 8; Gaps 1;

THIS PAGE BLANK (USPTO)

Result No.	Score	Query		Length	DB	ID	Description
		Match	\$				
1	1087	100.0		198	4	US-09-612-033B-8	Sequence 8, Appli
2	962	88.5		398	4	US-09-612-033B-14	Sequence 14, Appl
3	956	87.9		180	4	US-09-612-033B-10	Sequence 10, Appl
4	748	68.8		133	4	US-09-612-033B-6	Sequence 6, Appli
5	746.5	68.7		176	3	US-09-411-722-1	Sequence 1, Appli
6	746.5	68.7		176	4	US-09-855-266A-1	Sequence 1, Appli
7	682.5	62.8		148	3	US-09-411-722-2	Sequence 2, Appli
8	682.5	62.8		148	4	US-09-855-266A-2	Sequence 2, Appli
9	218.5	20.1		327	3	US-09-290-640-66	Sequence 66, Appl
10	218.5	20.1		327	4	US-09-665-615B-66	Sequence 66, Appl
11	212.5	19.5		123	4	US-09-855-266A-13	Sequence 13, Appl
12	208.5	19.2		355	1	US-08-292-549-6	Sequence 6, Appli
13	208.5	19.2		355	3	US-09-006-353A-14	Sequence 14, Appli
14	208.5	19.2		355	4	US-09-573-986-14	Sequence 14, Appli
15	207.5	19.1		285	3	US-08-804-166-6	Sequence 6, Appli
16	207.5	19.1		285	3	US-08-910-991-6	Sequence 6, Appli
17	207.5	19.1		285	4	US-09-756-186-6	Sequence 2, Appli
18	203.5	18.7		256	3	US-08-804-166-2	Sequence 2, Appli
19	203.5	18.7		256	3	US-08-910-991-2	Sequence 2, Appli
20	203.5	18.7		256	4	US-09-756-186-2	Sequence 2, Appli
21	203.5	18.7		307	3	US-08-804-166-4	Sequence 4, Appli
22	203.5	18.7		307	3	US-08-910-991-4	Sequence 4, Appli
23	203.5	18.7		307	4	US-09-756-186-4	Sequence 4, Appli
24	203.5	18.7		336	3	US-08-804-166-8	Sequence 8, Appli
25	203.5	18.7		336	3	US-08-910-991-8	Sequence 8, Appli
26	203.5	18.7		336	4	US-09-756-186-8	Sequence 8, Appli
27	202.5	18.6		199	1	US-08-050-319B-48	Sequence 48, Appl

```
; TITLE OF INVENTION: tms2, a No. 6627199el Member of the TNF-Receptor Superfamily
; TITLE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
US-09-612-033B-14

Query Match      88.5%; Score 962; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.6e-81;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSFKCPAGEYWSKDVC 60
Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSFKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTTEKONYLDACILCSTCDKQEMVADCSATS 120
Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTTEKONYLDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRTGLYYDPKFPESCRCPTCKPQGPVLQECNSTANTVCSSSVN 171
Db 121 DRKQCRTGLYYDPKFPESCRCPTCKPQGPVLQECNSTANTVCSSSVN 171

RESULT 3
US-09-612-033B-10
; Sequence 10, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tms2, a No. 6627199el Member of the TNF-Receptor Superfamily
; TITLE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-612-033B-10

Query Match      87.9%; Score 956; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.8e-81;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSFKCPAGEYWSKDVC 60
Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSFKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTTEKONYLDACILCSTCDKQEMVADCSATS 120
Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTTEKONYLDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRTGLYYDPKFPESCRCPTCKPQGPVLQECNSTANTVCSSSVN 170
Db 121 DRKQCRTGLYYDPKFPESCRCPTCKPQGPVLQECNSTANTVCSSSVN 170
```

```
RESULT 4
US-09-612-033B-6
; Sequence 6, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tms2, a No. 6627199el Member of the TNF-Receptor Superfamily
; TITLE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-612-033B-6

Query Match      68.8%; Score 748; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 8.1e-62;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSFKCPAGEYWSKDVC 60
Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSFKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTTEKONYLDACILCSTCDKQEMVADCSATS 120
Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTTEKONYLDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRTGLYY 133
Db 121 DRKQCRTGLYY 133

RESULT 5
US-09-411-722-1
; Sequence 1, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501/040001
; CURRENT APPLICATION NUMBER: US/09/411,722
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-1

Query Match      68.7%; Score 746.5; DB 3; Length 176;
Best Local Similarity 75.1%; Pred. No. 1.5e-61;
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;

Qy 7 SLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSFKCPAGEYWSKDVCCKNC 66
Db 5 SHVSSLSHWF-----LLLLLLNLFPLVIFAMPESYFNCPPDGEYQSNVDVCKTCPSG 56

Qy 67 TFVKAPCEIPHTQGCCKCHPGTFTTEKONYLDACILCSTCDKQEMVADCSATSDRKQC 126
```



```

Db 57 TFKVAPCKIPIHTQGCCKCHPGFTGKNGLHDCSTCDKQNMWVADCSATSDRKCBC 116
Qy 127 RTGLYYDDPKFPSCRCCTKCPQIGIPVLQECNSTANTVCSSSVSNPNRNLFLLLSPLSVL 186
Db 117 QIGLYYYDDPKFPSCRCCTKCPQIGIPVLQECNSTANTVCSSSVSNPNRNLFLLM----- 170
Qy 187 IVSVVVFRI 195
Db 171 ---LIVFCI 176

RESULT 6
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-1

Query Match 68.7%; Score 746.5; DB 4; Length 176;
Best Local Similarity 75.1%; Pred. No. 1.5e-61;
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;

Qy 7 SLVSSLRWFLRRLRLLLLLLNLPLOVKFAMLEHSPKCPAGEYWSKDVCKKCSAG 66
Db 5 SHVSSLSHW------LRLLLNLPVIFAMPESYSFNCPSGPDGEYQSDVCKCTCPG 56
Qy 67 TFKVAPCKIPIHTQGCCKCHPGFTGKNGLHDCSTCDKQNMWVADCSATSDRKCQC 126
Db 57 TFKVAPCKIPIHTQGCCKCHPGFTGKNGLHDCSTCDKQNMWVADCSATSDRKCBC 116
Qy 127 RTGLYYDDPKFPSCRCCTKCPQIGIPVLQECNSTANTVCSSSVSNPNRNLFLLLSPLSVL 186
Db 117 QIGLYYYDDPKFPSCRCCTKCPQIGIPVLQECNSTANTVCSSSVSNPNRNLFLLM----- 170
Qy 187 IVSVVVFRI 195
Db 171 ---LIVFCI 176

RESULT 7
US-09-411-722-2
; Sequence 2, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501/040001
; CURRENT APPLICATION NUMBER: US/09/411,722
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-2

Query Match 62.8%; Score 682.5; DB 3; Length 148;
Best Local Similarity 78.3%; Pred. No. 1e-55;
Matches 123; Conservative 8; Mismatches 17; Indels 9; Gaps 1;

Qy 39 AMLEHSPKCPAGEYWSKDVCKKCSAGTFVKAPCIPIHTQGCCKCHPGFTGKNGLH 98
Db 1 AMPESYSFNCPSGPDGEYQSDVCKCTCPSGTFVKAPCIPIHTQGCCKCHPGFTGKNGLH 60
Qy 99 ACILCSTCDKQNMWVADCSATSDRKCQCRGLYYDDPKFPSCRCCTKCPQIGIPVLQECN 158
Db 61 DCELCSTCDKQNMWVADCSATSDRKCCECQIGLYYYDDPKFPSCRCCTKCPQIGIPVLQECN 120
Qy 159 STANTVCSSSVSNPNRNLFLLLSPLSVLVVVFRI 195
Db 121 STANTVCSSSVSNPNRNLFLLM-----LIVFCI 148

RESULT 8
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-2

Query Match 62.8%; Score 682.5; DB 4; Length 148;
Best Local Similarity 78.3%; Pred. No. 1e-55;
Matches 123; Conservative 8; Mismatches 17; Indels 9; Gaps 1;

Qy 39 AMLEHSPKCPAGEYWSKDVCKKCSAGTFVKAPCIPIHTQGCCKCHPGFTGKNGLH 98
Db 1 AMPESYSFNCPSGPDGEYQSDVCKCTCPSGTFVKAPCIPIHTQGCCKCHPGFTGKNGLH 60
Qy 99 ACILCSTCDKQNMWVADCSATSDRKCQCRGLYYDDPKFPSCRCCTKCPQIGIPVLQECN 158
Db 61 DCELCSTCDKQNMWVADCSATSDRKCCECQIGLYYYDDPKFPSCRCCTKCPQIGIPVLQECN 120
Qy 159 STANTVCSSSVSNPNRNLFLLLSPLSVLVVVFRI 195
Db 121 STANTVCSSSVSNPNRNLFLLM-----LIVFCI 148

RESULT 9
US-09-290-640-66
; Sequence 66, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
```

```

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-2

Query Match 62.8%; Score 682.5; DB 3; Length 148;
Best Local Similarity 78.3%; Pred. No. 1e-55;
Matches 123; Conservative 8; Mismatches 17; Indels 9; Gaps 1;

Qy 39 AMLEHSPKCPAGEYWSKDVCKKCSAGTFVKAPCIPIHTQGCCKCHPGFTGKNGLH 98
Db 1 AMPESYSFNCPSGPDGEYQSDVCKCTCPSGTFVKAPCIPIHTQGCCKCHPGFTGKNGLH 60
Qy 99 ACILCSTCDKQNMWVADCSATSDRKCQCRGLYYDDPKFPSCRCCTKCPQIGIPVLQECN 158
Db 61 DCELCSTCDKQNMWVADCSATSDRKCCECQIGLYYYDDPKFPSCRCCTKCPQIGIPVLQECN 120
Qy 159 STANTVCSSSVSNPNRNLFLLLSPLSVLVVVFRI 195
Db 121 STANTVCSSSVSNPNRNLFLLM-----LIVFCI 148

RESULT 8
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-2

Query Match 62.8%; Score 682.5; DB 4; Length 148;
Best Local Similarity 78.3%; Pred. No. 1e-55;
Matches 123; Conservative 8; Mismatches 17; Indels 9; Gaps 1;

Qy 39 AMLEHSPKCPAGEYWSKDVCKKCSAGTFVKAPCIPIHTQGCCKCHPGFTGKNGLH 98
Db 1 AMPESYSFNCPSGPDGEYQSDVCKCTCPSGTFVKAPCIPIHTQGCCKCHPGFTGKNGLH 60
Qy 99 ACILCSTCDKQNMWVADCSATSDRKCQCRGLYYDDPKFPSCRCCTKCPQIGIPVLQECN 158
Db 61 DCELCSTCDKQNMWVADCSATSDRKCCECQIGLYYYDDPKFPSCRCCTKCPQIGIPVLQECN 120
Qy 159 STANTVCSSSVSNPNRNLFLLLSPLSVLVVVFRI 195
Db 121 STANTVCSSSVSNPNRNLFLLM-----LIVFCI 148

RESULT 9
US-09-290-640-66
; Sequence 66, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
```

```

; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-290-640-66

Query Match      20.1%; Score 218.5; DB 3; Length 327;
Best Local Similarity 30.0%; Pred. No. 1.9e-12;
Matches 57; Conservative 30; Mismatches 74; Indels 29; Gaps 8;

QY 32 LPLQVKFAMLEH-----SEK-----CPAGEYWSKDVCKKNCASGTFVKA 71
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 LPLVLASQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGGPCCQPGKXKVE 67
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 PCEIPHTQGCQKCHPG-TFTEKONYLDACILCTCDKQ--EMVADCSATSDRKCCORT 128
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 DCKNNGGTPTCAPCTEGEYMDKNHYADKRCRTLCDEHGLEVETNCTLTQNTKCKXP 127
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 GLYYDPKPPSCRPCTKCPGIPVLQECNSTANTVCSSSVSNPRNRLFLLSPLSLIV 188
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 D-FYCDSPGCEHVCASCSEHG--TLEPCTATSNCRK--QSPRNLW-LLTILVLLIP 181
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 SVVVFRIIR 198
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 LVFIYRKYRK 191

RESULT 10
US-09-665-615B-66
; Sequence 66, Application US/09665615B
; Patent No. 6653133
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-665-615B-66

Query Match      20.1%; Score 218.5; DB 4; Length 327;
Best Local Similarity 30.0%; Pred. No. 1.9e-12;
Matches 57; Conservative 30; Mismatches 74; Indels 29; Gaps 8;

QY 32 LPLQVKFAMLEH-----SEK-----CPAGEYWSKDVCKKNCASGTFVKA 71
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 LPLVLASQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQGGPCCQPGKXKVE 67
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 PCEIPHTQGCQKCHPG-TFTEKONYLDACILCTCDKQ--EMVADCSATSDRKCCORT 128
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 DCKNNGGTPTCAPCTEGEYMDKNHYADKRCRTLCDEHGLEVETNCTLTQNTKCKXP 127
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 GLYYDPKPPSCRPCTKCPGIPVLQECNSTANTVCSSSVSNPRNRLFLLSPLSLIV 188
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 D-FYCDSPGCEHVCASCSEHG--TLEPCTATSNCRK--QSPRNLW-LLTILVLLIP 181
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 SVVVFRIIR 198
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Db 182 LVFIYRKYRK 191
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 11
US-09-855-266A-13
; Sequence 13, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 08501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-13

Query Match      19.5%; Score 212.5; DB 4; Length 123;
Best Local Similarity 34.7%; Pred. No. 2.3e-12;
Matches 43; Conservative 15; Mismatches 59; Indels 7; Gaps 4;

QY 48 CPAGEY---WSKDVCKKNCAGTFVKAPCIPIHTQGCQKCHPGTFTEKONYLDACILCS 104
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 CPGGKYVHSKNSISCTCKCHKGYLVSDCPSPGSDTVCRCEKGTFTTASQNYLQCLSK 60
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 105 TCDKD--QEMVADCSATSDRKCCQRTGLYY-YDPKFPESCRCPTKCPGIPVLQECNSTA 161
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 TCRKMSQVEISPCQADKDTVCGCKENQFORLYSETHFQCVDCSPCFNG-TVTIPCKETQ 119
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 162 NTVC 165
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 NTVC 123

RESULT 12
US-08-292-549-6
; Sequence 6, Application US/08292549
; Patent No. 5464938
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,549
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/963,330

```

```
; FILING DATE: 10/19/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2602-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-292-549-6

Query Match 19.2%; Score 208.5; DB 1; Length 355;
Best Local Similarity 33.8%; Pred. No. 1.7e-11;
Matches 51; Conservative 21; Mismatches 68; Indels 11; Gaps 6;

QY 21 LLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCKKNCAGTFVKAPCEI-PHTQ 79
Db 7 LLLLSCLIIINSIDITPH----EPSNGKCKDNEYKXHLCLCLSCPPGTYASRLCDKSKNTN 62
QY 80 GQCEKCHPGTFTKDNVLDACILCS-TCDDQEMVADCSATSDRKQCORTGLYYDPKFP 138
Db 63 TQCTPCASDTFTSRNNHLPACLSNGRCDSNQVETRSCNTHNRICDCAPG-YVCFKLS 121
QY 139 ESCRPC---TKCPQGIPLVQECNSTANTVCS 166
Db 122 SGCKACVSQTKCGIGYGVSGH-TPTGDVWCS 151

RESULT 13
US-09-006-353A-14
; Sequence 14, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-PEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: protein
; US-09-006-353A-14

Query Match 19.2%; Score 208.5; DB 3; Length 355;
Best Local Similarity 33.8%; Pred. No. 1.7e-11;
Matches 51; Conservative 21; Mismatches 68; Indels 11; Gaps 6;

QY 21 LLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCKKNCAGTFVKAPCEI-PHTQ 79
Db 7 LLLLSCLIIINSIDITPH----EPSNGKCKDNEYKXHLCLCLSCPPGTYASRLCDKSKNTN 62
QY 80 GQCEKCHPGTFTKDNVLDACILCS-TCDDQEMVADCSATSDRKQCORTGLYYDPKFP 138
Db 63 TQCTPCASDTFTSRNNHLPACLSNGRCDSNQVETRSCNTHNRICDCAPG-YVCFKLS 121
QY 139 ESCRPC---TKCPQGIPLVQECNSTANTVCS 166
Db 122 SGCKACVSQTKCGIGYGVSGH-TPTGDVWCS 151

RESULT 14
US-09-573-986-14
; Sequence 14, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Pei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-573-986-14

Query Match 19.2%; Score 208.5; DB 4; Length 355;
Best Local Similarity 33.8%; Pred. No. 1.7e-11;
Matches 51; Conservative 21; Mismatches 68; Indels 11; Gaps 6;

QY 21 LLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCKKNCAGTFVKAPCEI-PHTQ 79
Db 7 LLLLSCLIIINSIDITPH----EPSNGKCKDNEYKXHLCLCLSCPPGTYASRLCDKSKNTN 62
QY 80 GQCEKCHPGTFTKDNVLDACILCS-TCDDQEMVADCSATSDRKQCORTGLYYDPKFP 138
Db 63 TQCTPCASDTFTSRNNHLPACLSNGRCDSNQVETRSCNTHNRICDCAPG-YVCFKLS 121
QY 139 ESCRPC---TKCPQGIPLVQECNSTANTVCS 166
Db 122 SGCKACVSQTKCGIGYGVSGH-TPTGDVWCS 151

RESULT 15
US-08-804-166-6
; Sequence 6, Application US/08804166
; Patent No. 6193972
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
```

;
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-804-166-6

Query Match 19.1%; Score 207.5; DB 3; Length 285;
Best Local Similarity 34.4%; Pred. No. 1.7e-11;
Matches 53; Conservative 17; Mismatches 71; Indels 13; Gaps 6;

QY 20 RLLLLLLLLLNLPLQVKFAMLELHSPKCPAGEY---WSKDVCKNCAGTFVKAPCEI 75
Db 2 RLSLLAFGLLCLPLWQBSA-----DSVCPQGYIHPQNNISICCTKCHKGTLYLNDPCG 56

QY 76 PHTQGCCKCHPGTTEKDNVLDACILCSTCDKD--QEMVADCSATSDRKCCQRTGLY-Y 132
Db 57 PQQDTDCRECSGSFTASENHLRHLCLSCSKCKEMGQVEISSCTVDRTVCGCRKNQYRH 116

QY 133 YDPKPEPCRCCTKCPQGIPIVLOECNSTANTVCS 166
Db 117 YNSENLFOCFNCTCLNG--TVHLSQCKONTVCT 149

Search completed: September 9, 2005, 09:35:53
Job time : 127.81 secs

120

```
QY 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGPVLQECNSTANTVCSVSNPNRRLFLLL 180
DB 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGPVLQECNSTANTVCSVSNPNRRLFLLL 180
QY 181 SPLSVLIIVSVVFRIR 198
DB 181 SPLSVLIIVSVVFRIR 198

RESULT 2
US-10-622-407-14
; Sequence 14, Application US/10622407
; Publication No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANT: Satis, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US/10/622,407
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US 09/612,033
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
US-10-622-407-14

Query Match 88.5%; Score 962; DB 15; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.4e-76;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVC 60
DB 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVC 60
QY 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGPVLQECNSTANTVCSVSN 171
DB 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGPVLQECNSTANTVCSVSN 171

RESULT 3
US-10-622-407-10
; Sequence 10, Application US/10622407
; Publication No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANT: Satis, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US/10/622,407
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US 09/612,033
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-622-407-10

Query Match 68.8%; Score 748; DB 15; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.2e-58;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVC 60
DB 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVC 60
QY 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKQCRTGLYY 133
DB 121 DRKQCRTGLYY 133

RESULT 5
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
```

```
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-622-407-10

Query Match 87.9%; Score 956; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.6e-76;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVC 60
DB 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVC 60
QY 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGPVLQECNSTANTVCSVSN 170
DB 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGPVLQECNSTANTVCSVSN 170

RESULT 4
US-10-622-407-6
; Sequence 6, Application US/10622407
; Publication No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANT: Satis, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NO
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US/10/622,407
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US 09/612,033
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-622-407-6

Query Match 68.8%; Score 748; DB 15; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.2e-58;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVC 60
DB 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVC 60
QY 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKQCRTGLYY 133
DB 121 DRKQCRTGLYY 133

RESULT 5
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
```

; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-1

Query Match 68.7%; Score 746.5; DB 9; Length 176;
Best Local Similarity 75.1%; Pred. No. 9.3e-58;
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;
QY 7 SLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCKNCAG 66
DB 5 SHVSSLSHWF-----LLLLLLNLFPLVIFAMPESYSFNCPPGEGYQSDNDVCKTCPSG 56
QY 67 TFVKAPCEIPTHQOQCEKCHPGFTTEKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOQCEKCHPGFTTGKONGLHDCELCSTCDKQNMVADCSATSDRKCEC 116
QY 127 RTGLYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186
DB 117 QIGLYYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLM----- 170
QY 187 IVSVVVFRI 195
DB 171 ---LIVFCI 176

RESULT 6
US-10-193-616-8
; Sequence 8, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-193-616-8

Query Match 68.7%; Score 746.5; DB 14; Length 176;
Best Local Similarity 75.1%; Pred. No. 9.3e-58;
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;
QY 7 SLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCKNCAG 66
DB 5 SHVSSLSHWF-----LLLLLLNLFPLVIFAMPESYSFNCPPGEGYQSDNDVCKTCPSG 56
QY 67 TFVKAPCEIPTHQOQCEKCHPGFTTEKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOQCEKCHPGFTTGKONGLHDCELCSTCDKQNMVADCSATSDRKCEC 116
QY 127 RTGLYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186
DB 117 QIGLYYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLM----- 170

QY 187 IVSVVVFRI 195
DB 171 ---LIVFCI 176

RESULT 7
US-10-802-332-1
; Sequence 1, Application US/10802332
; Publication No. US20040152879A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/10/802,332
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: US/09/855,266
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-802-332-1

Query Match 68.7%; Score 746.5; DB 16; Length 176;
Best Local Similarity 75.1%; Pred. No. 9.3e-58;
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;
QY 7 SLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCKNCAG 66
DB 5 SHVSSLSHWF-----LLLLLLNLFPLVIFAMPESYSFNCPPGEGYQSDNDVCKTCPSG 56
QY 67 TFVKAPCEIPTHQOQCEKCHPGFTTEKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOQCEKCHPGFTTGKONGLHDCELCSTCDKQNMVADCSATSDRKCEC 116
QY 127 RTGLYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186
DB 117 QIGLYYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLM----- 170
QY 187 IVSVVVFRI 195
DB 171 ---LIVFCI 176

RESULT 8
US-10-193-616-14
; Sequence 14, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14

```
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: ymkz5-Fc fusion protein
US-10-193-616-14

Query Match      65.4%; Score 711; DB 14; Length 396;
Best Local Similarity 80.0%; Pred. No. 2.8e-54;
Matches 132; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

Qy 7 SLVSSLSRWFLWRRLLLLLLLLLLNLPQVKFAMLEHSPKCPAGEYWSKDVCCCKNSAG 66
Db 5 SHVSSLSHWF-----LLLLLLLFLPVIFAMPESYSFNCPCGEYQSDNVCCCTCPSG 56

Qy 67 TFVKAPCEIPHTQGCCKCHPGTFTTEKDNLYDLCILCSTCDKQDMVADCSATSDRKQC 126
Db 57 TFVKAPCKIPHTQGCCKCHPGTFTGKDNGLHDCELCSTCDKQDMVADCSATSDRKCEC 116

Qy 127 RTGLYYDPKPPESCRCPTKCPQIGIPVLQECNSTANTVVCSSSVN 171
Db 117 QIGLYYDPKPPESCRCPTKCPQIGIPVLQECNSTANTVVCSSSVN 161

RESULT 9
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-2

Query Match      62.8%; Score 682.5; DB 9; Length 148;
Best Local Similarity 78.3%; Pred. No. 3.3e-52;
Matches 123; Conservative 8; Mismatches 17; Indels 9; Gaps 1;

Qy 39 AMLEHSPKCPAGEYWSKDVCCCKNSAGTFVKAPCEIPHTQGCCKCHPGTFTTEKDNLYD 98
Db 1 AMPESYSFNCPCGEYQSDNVCCCTCPSGTFVKAPCKIPHTQGCCKCHPGTFTGKDNGLH 60

Qy 99 ACILCSTCDKQDMVADCSATSDRKQCQRTGLYYDPKPPESCRCPTKCPQIGIPVLQECN 158
Db 61 DCELCSTCDKQDMVADCSATSDRKCECQIGLYYDPKPPESCRCPTKCPQIGIPVLQECN 120

Qy 159 STANTVCCSSSVNPRNRLFLLLSPLSVLIVSVVVFRI 195
Db 121 STANTVCCSSSVNPRNWLFLM-----LIVFCI 148

RESULT 11
US-10-193-616-6
; Sequence 6, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-193-616-6

Query Match      43.0%; Score 467; DB 14; Length 117;
Best Local Similarity 73.6%; Pred. No. 2.3e-33;
Matches 89; Conservative 5; Mismatches 19; Indels 8; Gaps 1;

Qy 7 SLVSSLSRWFLWRRLLLLLLLLLLNLPQVKFAMLEHSPKCPAGEYWSKDVCCCKNSAG 66
Db 5 SHVSSLSHWF-----LLLLLLLFLPVIFAMPESYSFNCPCGEYQSDNVCCCTCPSG 56

Qy 67 TFVKAPCEIPHTQGCCKCHPGTFTTEKDNLYDLCILCSTCDKQDMVADCSATSDRKQC 126
Db 57 TFVKAPCKIPHTQGCCKCHPGTFTGKDNGLHDCELCSTCDKQDMVADCSATSDRKCEC 116
```



```

; LENGTH: 454
; TYPE: PRT
; ORGANISM: Mus musculus
UUS-10-410-012-3

```

```
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37677
; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-948-018-18

Query Match      20.1%; Score 218.5; DB 9; Length 204;
Best Local Similarity 30.0%; Pred. No. 2.9e-11;
Matches 57; Conservative 30; Mismatches 74; Indels 29; Gaps 8;

Qy 32 LPLOVKFAMLELH-----SPK-----CPAGEYWSKDVCKKNCASAGTFVKA 71
Db 8 LPLVLGSQLRVHTQGTNSISESLKRRRVHETDKNCSEGLYQGPGFCCQCPQFGKKVE 67

Qy 72 PCEIPHTQGOCEKCHPG--TFTEKDYLDACILCTCDKQD--EMVADCSATSDRKCOCRT 128
Db 68 DCKMNGGTPTCAPCTEGKEYMDKNHYADKCRCTLCDDEHGLEVEVTNCTLTQNTKCKCP 127

Qy 129 GLYYDPKFPESCRPCTKCPGIPVLOECNSTANTVCGSSVSVNPRNRLFLLLSLSLVLI 188
Db 128 D-FYCDSPGCEHCVRASCSEHG--TLEPCTATSNINCRK--QSPRRLW-LTLTLLVLLIP 181

Qy 189 SVVVFRIIR 198
Db 182 LVFIYRKYRK 191
```

Search completed: September 9, 2005, 09:55:17
Job time : 603.905 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2005, 06:50:20 ; Search time 143.524 Seconds
(without alignments)
132.737 Million cell updates/sec

Title: US-10-622-407-8
Perfect score: 1087
Sequence: 1 MFGFFCSLVSSLSRWFLWRR.....LLSPLSVLIVVVVFIIRR 198
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	226	20.8	454	1 GQMS1	tumor necrosis fac
2	218.5	20.1	327	2 A46484	apoptosis-mediati
3	212.5	19.5	461	1 GQRT1	tumor necrosis fac
4	210	19.3	324	2 JC2395	Fas antigen precu
5	201.5	18.5	348	2 T28623	hypothetical prote
6	201.5	18.5	349	2 D36858	gene G4R protein -
7	201.5	18.5	349	2 D72175	G2R protein - vari
8	201.5	18.5	455	1 GQHUT1	tumor necrosis fac
9	200.5	18.4	461	2 JC4302	tumor necrosis fac
10	188	17.3	427	1 GQHUN	nerve growth facto
11	186.5	17.2	271	2 S12783	OX40 antigen precu
12	183.5	16.9	335	2 A40036	apoptosis-mediati
13	180.5	16.6	651	2 JC7705	death receptor-6 -
14	176.5	16.2	416	1 JN0006	nerve growth facto
15	175	16.1	314	2 I37393	FAS soluble protei
16	175	16.1	425	1 A26431	nerve growth facto
17	173.5	16.0	325	2 B43692	T2 protein - rabbi
18	173.5	16.0	461	1 A35356	tumor necrosis fac
19	167.5	15.4	326	1 GQVZML	T2 protein - myxom
20	162	14.9	272	2 I48700	gene ox40 protein
21	158.5	14.6	435	2 I54182	tumor necrosis fac
22	157.5	14.5	260	1 A46517	CD27 antigen precu
23	156	14.4	474	2 B38634	tumor necrosis fac
24	151.5	13.9	250	1 A49053	CD27 antigen precu
25	151.5	13.9	459	2 I48854	gene murine tumour
26	151	13.9	595	2 A42086	CD30 antigen precu
27	143	13.2	277	2 I37552	OX40 homology - hum
28	126	11.6	1790	1 MWFF91	laminin beta-1 cha
29	123	11.3	256	2 B32393	T-cell antigen 4-1

30 122 11.2 305 2 A46476 B cell-associated
31 121.5 11.2 493 2 JC5486 membrane glycoprot
32 120.5 11.1 255 2 I38426 lymphocyte activat
33 119.5 11.0 3635 2 T10053 laminin alpha 5 ch
34 116 10.7 1193 2 A44018 laminin B2t chain
35 116 10.7 4391 2 A38096 perlecan precursor
36 114.5 10.5 1801 1 MMRTS laminin beta-2 cha
37 114 10.5 1339 2 JC4387 epidermal growth f
38 112 10.3 3707 2 S18252 heparan sulfate pr
39 111.5 10.3 1609 1 MMHUB2 laminin gamma-1 ch
40 111.5 10.3 4545 1 S25111 alpha-2-macroglobu
41 111 10.2 1372 2 T25933 hypothetical prote
42 111 10.2 1548 2 S34583 serine proteinase
43 111 10.2 1786 1 MMWSB1 laminin beta-1 cha
44 110.5 10.2 713 2 A35502 major surface-labe
45 110 10.1 1192 2 S69000 laminin gamma 2 ch

ALIGNMENTS

RESULT 1

GQMS1

tumor necrosis factor receptor 1 precursor - mouse

N;Alternate names: tumor necrosis factor receptor, 55K

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence,revision 30-Jun-1992 #text change 09-Jul-2004

C;Accession: A38634; B40254; S16677; S19021; I54532; I57826

R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.;

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r

A;Reference number: A38634; MUID:91187885; PMID:1849278

A;Accession: A38634

A;Molecule type: mRNA

A;Residues: 1-454 <LEU>

A;Cross-references: UNIPROT:P25118; GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826

R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk

Mol. Cell. Biol. 11, 3020-3026, 1991

A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A;Reference number: A40254; MUID:91246168; PMID:1645445

A;Accession: B40254

A;Molecule type: mRNA

A;Residues: 1-454 <GO2>

A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826

R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissenerghis, A.M.; Gray, P.W.; Feldma

Eur. J. Immunol. 21, 1649-1656, 1991

A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis

A;Reference number: S16677; MUID:91285014; PMID:1647956

A;Accession: S16677

A;Molecule type: mRNA

A;Residues: 1-454 <BAR>

A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579

R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.

Immunogenetics 34, 338-340, 1991

A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.

A;Reference number: S19021; MUID:92039815; PMID:1657766

A;Accession: S19021

A;Molecule type: mRNA

A;Residues: 1-454 <ROT>

A;Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849

R;Bebo, B.F.

Immunogenetics 39, 450-451, 1994

A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1

A;Reference number: I54532; MUID:94245292; PMID:8188324

A;Accession: I54532

A;Status: translated from GB/EMBL/DBU

A;Molecule type: mRNA

A;Residues: 1-454 <RES>

A;Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733

R;Rothe, J.G.; Bluetmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.

Mol. Immunol. 30, 165-176, 1993

A;Title: Genomic organization and promoter function of the murine tumor necrosis factor

A;Reference number: I57826; MUID:93156721; PMID:8381516

RESULT 4

JC2395
 Fas antigen precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: JC2395; PC2246
 R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
 Biochem. Biophys. Res. Commun. 198, 666-674, 1994
 A;Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver
 A;Reference number: JC2395; MUID:94128114; PMID:7507668
 A;Accession: JC2395
 A;Molecule type: mRNA
 A;Residues: 1-324 <KIM>
 A;Cross-references: UNIPROT:Q63199; DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005
 A;Experimental source: thymus
 A;Accession: PC2246
 A;Molecule type: mRNA
 A;Residues: 1-62, 'RFT' <K12>
 A;Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489
 A;Experimental source: liver
 C;Genetics:
 A;Introns: 62/1
 C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
 C;Keywords: transmembrane protein
 F;1-21/Domain: signal sequence predicted <SIG>
 F;22-324/Product: Fas antigen #status predicted <MAT>
 F;44-79/Domain: NGF receptor repeat homology <NGF>
 F;81-124/Domain: NGF receptor repeat homology <NG4>
 F;171-188/Domain: transmembrane #status predicted <TM>

Query Match 19.3%; Score 210; DB 2; Length 324;
 Best Local Similarity 29.4%; Pred. No. 9.1e-09;
 Matches 57; Conservative 30; Mismatches 79; Indels 28; Gaps 9;

QY 17 LWRRLRLRLRLRLPLQVY-----FAMLELH-----SFKCPAGEYWSKDVCKNC 63
 DB 2 LW--IMAVLPLVAGPELVNRMQGTDSIFEGLELKRVSRETNNCSGLYQVGFCCQPC 59
 QY 64 SAGTFVKAPCEIPTHQGCCKCHPGT---FTEKDNVLDACILCSTCKDQ--EMVADCS 117
 DB 60 QPGERKVKDCT---TSGAPTCPTGEBEYTRKHYSKRCRCAPCDGEGHLEVTNCT 116
 QY 118 ATSDRKQCRTGLYYDPKFPESCRCPTCKPQGI-PVLQBCNSTANTVCSSSVSNPNRL 176
 DB 117 RTQNTKCRKEN-PYCNASLCDHCYHCTSC--GLEDLLEPCTRTSNTKCKKQSSNYKLW 173
 QY 177 FLLSLPLSVLIVSV 190
 DB 174 LLILPLGLAILFVFI 187

RESULT 5

T28623
 hypothetical protein G2R - variola major virus
 C;Species: variola major virus
 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T28623
 R;Masung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
 Nature 366, 748-751, 1993
 A;Title: Potential virulence determinants in terminal regions of variola smallpox virus
 A;Reference number: 220488; MUID:94088747; PMID:8264798
 A;Accession: T28623
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-348 <MAS>
 A;Cross-references: UNIPROT:P34015; EMBL:I22579; NID:g623595; PIDN:AAA60933.1; PID:g4391
 A;Experimental source: strain Bangladesh 1975
 C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 18.5%; Score 201.5; DB 2; Length 348;
 Best Local Similarity 35.5%; Pred. No. 4.1e-08;

Matches 44; Conservative 18; Mismatches 55; Indels 7; Gaps 5;
 QY 47 KCPAGEYWSKDVCKNCAGTFVKAPCEIPTHQGCCKCHPGTFTKDNVLDACILCS-T 105
 DB 30 KCKDTEYKRHNLCCLSPPGTYASRLCD-SKNTQTCTPCGSGTFTSRNNHLPACLSNGR 88
 QY 106 CDKDOEMVADCSATSDRKQCRTGLYYDPKFPESCRCPC---TKCPQGIPLVQECNSTAN 162
 DB 89 CNSNOVETRSCTNTHNRICECSPG-YVCLLKSGSGCKACVSTQTKCGIGYGVSGH-TSVGD 146
 QY 163 TVCS 166
 DB 147 VICS 150

RESULT 6

D36858
 gene G4R protein - variola virus
 N;Alternate names: B28R protein (COP)
 C;Species: variola virus
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: D36858; S46888; S32385; S35987
 R;Blinov, V.M.
 submitted to GenBank, November 1992
 A;Reference number: A36859
 A;Accession: D36858
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-349 <BLI>
 A;Cross-references: UNIPROT:P34015; GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
 A;Experimental source: strain India-1967, ssp. major, isolate Ind3
 R;Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnjakov, S.G.; Chizhikov, V.E.; Frolov
 submitted to the EMBL Data Library, April 1992
 A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
 A;Reference number: S46868
 A;Accession: S46888
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-349 <ROL>
 A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
 A;Experimental source: strain India-1967, isolate Ind3
 R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
 FEBS Lett. 319, 80-83, 1993
 A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
 A;Reference number: S32385; MUID:93202281; PMID:8384129
 A;Accession: S32385
 A;Molecule type: DNA
 A;Residues: 31-168 <SHC>
 A;Cross-references: EMBL:X69198
 A;Experimental source: strain India-1967, ssp. major
 C;Genetics:
 A;Gene: G4R
 C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
 F;32-66/Domain: NGF receptor repeat homology <NGF>
 F;68-109/Domain: NGF receptor repeat homology <NG2>
 F;110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 18.5%; Score 201.5; DB 2; Length 349;
 Best Local Similarity 35.5%; Pred. No. 4.1e-08;
 Matches 44; Conservative 18; Mismatches 55; Indels 7; Gaps 5;

QY 47 KCPAGEYWSKDVCKNCAGTFVKAPCEIPTHQGCCKCHPGTFTKDNVLDACILCS-T 105
 DB 31 KCKDTEYKRHNLCCLSPPGTYASRLCD-SKNTQTCTPCGSGTFTSRNNHLPACLSNGR 89
 QY 106 CDKDOEMVADCSATSDRKQCRTGLYYDPKFPESCRCPC---TKCPQGIPLVQECNSTAN 162
 DB 90 CNSNOVETRSCTNTHNRICECSPG-YVCLLKSGSGCKACVSTQTKCGIGYGVSGH-TSVGD 147
 QY 163 TVCS 166
 DB 148 VICS 151

A;Accession: JC2404
A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and C;Genetics:
A;Gene: GDB:TNFR1
A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 18.5%; Score 201.5; DB 1; Length 455;
Best Local Similarity 30.6%; Pred. No. 5e-08;
Matches 49; Conservative 21; Mismatches 73; Indels 17; Gaps 5;
QY 23 LLLALLLLNLPLQV-----KFMALHSPKCPAGEY---WSKDVCKKCSAGTFV 69
DB 9 LLLPLVLLLELVGYPGVTGLVPHLGDRKRDVSPQGYIHPQNNISCTCKHKGTYL 68
QY 70 KAPCEIPHTQGCCKHPGFTTEKDYNDACILCTCDKD--QEMVADCSATSDRKQCCR 127
DB 69 YNDCPQPGQDTCRECSGSFTASENHLRHLCSCKRKEMGQVEISSCTVDRDVTGCCR 128
QY 128 TGLY-YDPRFPSPCRCTKCPQIGPVLQECNSTANTVCS 166
DB 129 KQVRYHWSNLFQCFNCSLCNG-TVHLSCQEKQNTVCT 167
RESULT 9
JC4302
tumor necrosis factor receptor p55 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4302; PC4093
R;Suter, B.; Faull, U.
Gene 163, 263-266, 1995
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A;Reference number: JC4302; MUID:96011645; PMID:7590278
A;Accession: JC4302
A;Molecule type: mRNA
A;Residues: 1-461 <SUT>
A;Cross-references: UNIPROT:P50555; GB:U19994; NID:gl141752; PIDN:AAC48499.1; PID:gl1417
A;Accession: PC4093
A;Molecule type: protein
A;Residues: 1-7 <SU2>
A;Experimental source: kidney cell line 15
C;Genetics:
A;Gene: tnfr
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F;84-126/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NGF>
F;211-231/Domain: transmembrane #status predicted <TMW>
F;361-447/Domain: signal transduction #status predicted <SIT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 18.4%; Score 200.5; DB 2; Length 461;

Best Local Similarity 30.8%; Pred. No. 6e-08;
Matches 49; Conservative 25; Mismatches 70; Indels 15; Gaps 7;
QY 21 LLLALLLLLLNLPLQV-----ELHSPKCPAGEY---WSKDVCKKCSAGTFVKA 71
DB 11 LPLVLRALLVDVYPAGVHGLVHPGDRKRESLCPQGYSHPNRSICCTKCHKGIYLNH 70
QY 72 PCBIPHTQGCCKHPGFTTEKDYNDACILCTC--DKQEMVADCSATSDRKQCCR 129
DB 71 DCLGPGGLDTCRECDNGTFTASENHLTCLCSCKRSEMSQVBIPTVDRTVCGCRKN 130
QY 130 LY--YDPRFPSPCRCTKCPQIGPVLQECNSTANTVCS 166
DB 131 QVRKYWSETLQ-CLNCSLCPNG-TVOLPCLEKQDTICN 167
RESULT 10
QGHUN
nerve growth factor receptor precursor, low affinity [validated] - human
N;Alternate names: NGF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A25218; A60204; S21689; I57638
R;Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor.
A;Reference number: A25218; MUID:87051725; PMID:3022937
A;Accession: A25218
A;Molecule type: mRNA
A;Residues: 1-427 <JOH>
A;Cross-references: UNIPROT:P08138; GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205
R;Marano, N.; Dietzschold, B.; Barley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A;Reference number: A60204; MUID:87085574; PMID:3025363
A;Accession: A60204
A;Molecule type: protein
A;Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A;Experimental source: melanoma cell line A875
A;Note: this sequence has been corrected by a note added in proof to follow the nucleotide
R;Visavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor rec
A;Reference number: S21689; MUID:92198017; PMID:1372492
A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor
A;Reference number: I57638; MUID:89096903; PMID:2850481
A;Accession: I57638
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status predicted <EXT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>

RESULT 12
A40036
apoptosis-mediating surface antigen Fas precursor - human
N:Alternate names: surface antigen APO-1
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
C:Accession: A40036; S24543; A38142
R:Ittoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase,

death receptor-6 - chicken
C/Species: Gallus gallus (chicken)
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
C/Accession: JCT7705
R/Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A/Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A/Reference number: JCT7705; MUID:21308433; PMID:11414698
A/Accession: JCT7705
A/Molecule type: mRNA
A/Residues: 1-651 <BRI>
A/Cross-references: UNIPROT:Q98SM6; GB:AF349908
C/Comment: This receptor, a member of the tumor necrosis factor receptor fa
ctria, activates a cell death and/or survival signaling cascade.
C/Genetics:
A/Gene: dr-6
C/Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor

C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

Query Match 16.6%; Score 180.5; DB 2; Length 651;
Best Local Similarity 29.8%; Pred. No. 2.4e-06;
Matches 45; Conservative 27; Mismatches 66; Indels 13; Gaps 5;

Qy 22 LLLALLLLPLQVKFAMLELHSHFKCPAGRY-----WSKDVCKKNCAGTFVKAPCEI 75
Db 9 VLPLVLFLGTADAQPKLTS-EQNAVSLPAGKYLHLDRATNQELICDKCPAGTYVSKHC-T 66
Qy 76 PHTQCEKCHPGFTTEKDNLYLDACILC-STCDKQDQWVADCSATSDRKCOQRTGLYYDD 134
Db 67 KSTLRECSPCPDGFTFKHENGIERCHPCRPCELPMEIKTHCTALTDRCTCLSGTF--- 123
Qy 135 KPFPESCRCPTKCPQGIPLVQECNSTANTVC 165
Db 124 -QINDTCVPYTVCPVGVGVRKKGTEDEVRC 153

RESULT 14
JN0006
nerve growth factor receptor, low affinity precursor - chicken
N;Alternate names: NGF receptor
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JN0006; A60504
R;Large, T.H.; Weiskamp, G.; Heider, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid
Neuron 2, 1123-1134, 1989
A;Title: Structure and developmental expression of the nerve growth factor receptor in b
A;Reference number: JN0006; MUID:90166579; PMID:2560385
A;Accession: JN0006
A;Molecule type: mRNA
A;Residues: 1-416 <LAR>
A;Cross-references: UNIPROT:P18519
A;Experimental source: embryonic chick brain
R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, B.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A;Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; MUID:90152140; PMID:2154393
A;Accession: A60504
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HEU>
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; b
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-416/Product: nerve growth factor receptor #status predicted <MAT>
F;21-239/Domain: extracellular #status predicted <EXT>
F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
F;101-139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.2%; Score 176.5; DB 1; Length 416;
Best Local Similarity 30.7%; Pred. No. 3.4e-06;
Matches 43; Conservative 20; Mismatches 68; Indels 9; Gaps 4;

Qy 27 LLLALLPLQVKFAMLELHSHFKPAGEYWSKDVCKKNCAGTFVKAPCEIPIHTQCEKCH 86
Db 7 LLLLLPAGPTWGSKE-----KLTQNTTSGECCCKACNLGEGVQPCGV--NQTVCEPCL 60

C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

Query Match 16.6%; Score 180.5; DB 2; Length 651;
Best Local Similarity 29.8%; Pred. No. 2.4e-06;
Matches 45; Conservative 27; Mismatches 66; Indels 13; Gaps 5;

Qy 22 LLLALLLLPLQVKFAMLELHSHFKCPAGRY-----WSKDVCKKNCAGTFVKAPCEI 75
Db 9 VLPLVLFLGTADAQPKLTS-EQNAVSLPAGKYLHLDRATNQELICDKCPAGTYVSKHC-T 66
Qy 76 PHTQCEKCHPGFTTEKDNLYLDACILC-STCDKQDQWVADCSATSDRKCOQRTGLYYDD 134
Db 67 KSTLRECSPCPDGFTFKHENGIERCHPCRPCELPMEIKTHCTALTDRCTCLSGTF--- 123
Qy 135 KPFPESCRCPTKCPQGIPLVQECNSTANTVC 165
Db 124 -QINDTCVPYTVCPVGVGVRKKGTEDEVRC 153

RESULT 14
JN0006
nerve growth factor receptor, low affinity precursor - chicken
N;Alternate names: NGF receptor
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JN0006; A60504
R;Large, T.H.; Weiskamp, G.; Heider, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid
Neuron 2, 1123-1134, 1989
A;Title: Structure and developmental expression of the nerve growth factor receptor in b
A;Reference number: JN0006; MUID:90166579; PMID:2560385
A;Accession: JN0006
A;Molecule type: mRNA
A;Residues: 1-416 <LAR>
A;Cross-references: UNIPROT:P18519
A;Experimental source: embryonic chick brain
R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, B.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A;Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; MUID:90152140; PMID:2154393
A;Accession: A60504
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HEU>
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; b
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-416/Product: nerve growth factor receptor #status predicted <MAT>
F;21-239/Domain: extracellular #status predicted <EXT>
F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
F;101-139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.2%; Score 176.5; DB 1; Length 416;
Best Local Similarity 30.7%; Pred. No. 3.4e-06;
Matches 43; Conservative 20; Mismatches 68; Indels 9; Gaps 4;

Qy 27 LLLALLPLQVKFAMLELHSHFKPAGEYWSKDVCKKNCAGTFVKAPCEIPIHTQCEKCH 86
Db 7 LLLLLPAGPTWGSKE-----KLTQNTTSGECCCKACNLGEGVQPCGV--NQTVCEPCL 60

Qy 87 PG-TFTEKDNLYLDACILCSTCDKQDQWVADCSATSDRKCOQRTGLYYDDPKFPESCRCPT 145
Db 61 DSVTYSDDTVSATPCKPCKPCTQCVGLHSMSPAFVCSDDDAVCRCAYG--YFQDELGSGCKECS 118
Qy 146 KCPQGIPLVQECNSTANTVC 165
Db 119 ICEVGLMFPFCDSDQDTVC 138

RESULT 15
I37383
FAS soluble protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I37383
R;Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are
A;Reference number: I37383; MUID:95181785; PMID:7533181
A;Accession: I37383
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-314 <RES>
A;Cross-references: UNIPROT:P25445; EMBL:Z47993; NID:9728578; PIDN:CAA88031.1; PID:96955
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo

Query Match 16.1%; Score 175; DB 2; Length 314;
Best Local Similarity 31.6%; Pred. No. 3.6e-06;
Matches 36; Conservative 19; Mismatches 53; Indels 6; Gaps 4;

Qy 59 CCNCSAGTGVKAPCEIPIHTQCEKCHPG-TTFEKDNLYLDACILCSTCDKQ--EMVAD 115
Db 59 CHKPCPPGERKARDCTVNGDEPDVCPQCEGKYTDKAHFSKCRRCRLCDEGHGLEVIN 118
Qy 116 CSATSDRKCOQRTGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSV 169
Db 119 CTRTQNTYKCRKPN-FFCNSTVCEHCDPCTKCEHGI--IKECTLTSNTKKEEV 169

Search completed: September 9, 2005, 09:31:38
Job time : 144.524 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 23:31:32 ; Search time 740.143 Seconds
(without alignments)
136.989 Million cell updates/sec

Title: US-10-622-407-8

Perfect score: 1087

Sequence: 1 MFGFFCSLVSSLSRWFLWRR.....LLSPLSLVSVVVFRIIRR 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1087	100.0	198	1	TR22_MOUSE	Q9er62 mus musculus
2	746.5	68.7	176	1	TR23_MOUSE	Q9er63 mus musculus
3	320	29.4	204	1	TR26_MOUSE	P83626 mus musculus
4	303	27.9	438	2	Q9DFV0	Q9dfv0 brachydanio
5	286.5	26.4	225	2	Q7T3M7	Q7t3m7 gallus galli
6	286.5	26.4	410	2	Q7T3M8	Q7t3m8 gallus galli
7	284.5	26.2	395	2	Q800K8	Q800k8 paralichthy
8	280	25.8	357	2	Q9DF34	Q9df34 brachydanio
9	265.5	24.4	321	2	Q6DJ81	Q6dj81 xenopus tro
10	247	22.7	328	2	Q76B99	Q76b99 xenopus lae
11	246	22.6	328	2	Q6GL24	Q6gl24 xenopus lae
12	243.5	22.4	327	2	Q97491	Q97491 ovis aries
13	239.5	22.0	289	2	Q678B7	Q678b7 lymphocysti
14	239	22.0	189	2	Q95185	Q95185 felis silve
15	233	21.4	323	1	TNR6_BOVIN	P51867 bos taurus
16	233	21.4	446	2	Q95ND3	Q95nd3 felis silve
17	232	21.3	328	2	Q76B98	Q76b98 xenopus lae
18	226	20.8	440	2	Q6QHF0	Q6qh0 mus musculus
19	226	20.8	440	2	Q6QHF1	Q6qh1 mus musculus
20	226	20.8	454	1	TR1A_MOUSE	P25118 mus musculus
21	224.5	20.7	332	1	TNR6_PIG	Q77736 sus scrofa
22	224	20.6	319	2	Q9TW79	Q9tw79 oryctolagus
23	223	20.5	440	2	Q6QHF2	Q6qh2 mus musculus
24	221	20.3	347	2	Q57119	Q57119 cowpox viru
25	218.5	20.1	263	2	Q9XS60	Q9xs60 oryctolagus
26	218.5	20.1	320	2	Q9XS29	Q9xs29 oryctolagus
27	218.5	20.1	327	1	TNR6_MOUSE	P25446 mus musculus
28	216	19.9	189	2	Q9T530	Q9t530 canis famill
29	216	19.9	360	2	Q57118	Q57118 cowpox viru
30	215.5	19.8	326	2	Q57120	Q57120 cowpox viru
31	215.5	19.8	348	2	Q57103	Q57103 monkeypox v

32	215.5	19.8	348	2	Q57108	Q57108 monkeypox v
33	215.5	19.8	348	2	Q57277	Q57277 monkeypox v
34	215.5	19.8	349	2	Q57101	Q57101 monkeypox v
35	215.5	19.8	349	2	Q57102	Q57102 monkeypox v
36	215.5	19.8	349	2	Q57291	Q57291 monkeypox v
37	215.5	19.8	349	2	Q57305	Q57305 cowpox viru
38	215.5	19.8	349	2	Q57121	Q57121 cowpox viru
39	213.5	19.6	351	2	Q6WB14	Q6wb14 callithrix
40	213.5	19.6	326	2	Q57122	Q57122 cowpox viru
41	213.5	19.6	351	1	CRMB_COWPX	Q73559 cowpox viru
42	212.5	19.5	349	2	Q57099	Q57099 monkeypox v
43	212.5	19.5	389	2	Q6NUU6	Q6nuu6 brachydanio
44	212.5	19.5	461	1	TR1A_RAT	P22934 rattus norv
45	211.5	19.5	318	2	Q7T2H3	Q7t2h3 oncorhynch

ALIGNMENTS

RESULT 1

TR22_MOUSE STANDARD; PRT; 198 AA.

AC Q9ER62; Q8VHB9; Q9CZM4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 22 (Tumor necrosis factor receptor p60 homolog 2) (TNF receptor family member SOBA)
 DE (Decoy TRAIL receptor 2) (TNF receptor homolog 2)
 GN Name=Tnfrsf22; Synonyms=Dctrailr2, Tnfrh2, Tnfrsf1a2;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=129/Sv; TISSUE=Embryonic stem cells;
 RX MEDLINE=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691;
 RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R., Lane N., Reik W., Walter J.;
 RT "Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting.";
 RL Hum. Mol. Genet. 9:2691-2706(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND 3D-STRUCTURE MODELING OF 62-170.
 RC STRAIN=NIH Swiss;
 RX PubMed=12466268; DOI=10.1074/jbc.M210783200;
 RA Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M., Burkly L.C., Tschopp J., Zheng T.S.;
 RT "Identification of a new murine tumor necrosis factor receptor locus that contains two novel murine receptors for tumor necrosis factor-related apoptosis-inducing ligand (TRAIL).";
 RL J. Biol. Chem. 278:5444-5454(2003).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX Resser P., Mao W., Baldwin D.T., Pan G.;
 RT "Characterization of SOBA, a murine member of the TNFR family.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bratt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

FT	REPEAT	84	124	TNFR-Cys 2.
FT	REPEAT	125	165	TNFR-Cys 3.
FT	DISULFID	48	59	By similarity.
FT	DISULFID	60	73	By similarity.
FT	DISULFID	63	82	By similarity.
FT	DISULFID	85	100	By similarity.
FT	DISULFID	103	116	By similarity.
FT	DISULFID	106	124	By similarity.
FT	DISULFID	126	141	By similarity.
FT	DISULFID	144	157	By similarity.
FT	DISULFID	147	165	By similarity.
FT	CARBOHYD	62		N-linked (GlcNAc..) (Potential).
FT	CARBOHYD	158		N-linked (GlcNAc..) (Potential).
FT	VARSPLIC	171	198	NNPRNFLLLSPLSVLIVSVVVFRIIR -> RRSASVAMP I (in isoform 2). /FTId=VSP_007648. L -> V (in Ref. 2). L -> C (in Ref. 1); CAC16406).
SQ	SEQUENCE	198 AA;	22375 MW; BBF8F52961EA9983 CRC64;	
	Query Match	100.0%;	Score 1087; DB 1; Length 198;	
	Best Local Similarity	100.0%;	Pred. No. 3.4e-85;	Gaps 0;
	Matches 198; Conservative	0; Mismatches	0; Indels	0;
Qy	1	MFGFFCSLVSSLSRWFWRRLRLLLLLLLLNLPLQVKFAMLEHLSFKPAGEYWSKDVC	60	
Dd	1	MFGFFCSLVSSLSRWFWRRLRLLLLLLLLNLPLQVKFAMLEHLSFKPAGEYWSKDVC	60	
Qy	61	KNGSAGTFVKAPCEIPHTQGQCCKCHPGTTEKXNYLDACILCTCDKOEMVADCSATS	120	
Dd	61	KNGSAGTFVKAPCEIPHTQGQCCKCHPGTTEKXNYLDACILCTCDKOEMVADCSATS	120	
Qy	121	DRKCQRTGLYYVDPKFPESCRCPTCKCPGIPVLQECNSTANTVCCSSVSNPNRRLFLL	180	
Dd	121	DRKCQRTGLYYVDPKFPESCRCPTCKCPGIPVLQECNSTANTVCCSSVSNPNRRLFLL	180	
Qy	181	SPLSVLIVSVVVFRIIR	198	
Dd	181	SPLSVLIVSVVVFRIIR	198	
RESULT 2				
TR23 MOUSE				
ID	TR23_MOUSE	STANDARD;	PRT;	176 AA.
AC	O3RG3; O8VHC0;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 23 precursor (Tumor			
DE	necrosis factor receptor p60 homolog 1) (TNF receptor family member			
DE	SOB) (Decoy TRAIL receptor 1) (TNF receptor homolog 1).			
GN	Name=Tnfrsf23; Synonyms=Bctrailr1, Tnfrl1, Tnfrsfll1;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=129/Sv; TISSUE=Embryonic stem cells;			
RX	MEDLINE=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691;			
RA	Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,			
RA	Lane N., Reik W., Walter J.;			
RT	"Sequence and functional comparison in the Beckwith-Wiedemann region:			
RT	implications for a novel imprinting centre and extended imprinting.";			
RL	Hum. Mol. Genet. 9:2691-2706(2000).			
RP	[2]			
RP	SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND 3D-STRUCTURE			
RP	MODELING OF 52-160.			
RC	STRAN=C57BL/6;			
RK	PubMed=12468268; DOI=10.1074/jbc.M210783200;			
RA	Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A.,			
RA	Gong D., Dobles M., Hertzig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,			

Burkly L.C., Tschopp J., Zheng T.S.;
Identification of a new murine tumor necrosis factor receptor locus
that contains two novel murine receptors for tumor necrosis factor-
related apoptosis-inducing ligand (TRAIL).";
J. Biol. Chem. 278:5444-5454(2003).

[3]
SEQUENCE FROM N.A.
Pan G., Mao W., Risser P.;
Characterization of SOB, a member of the TNFR family.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -|- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Lacks a
cytoplasmic death domain and hence is not capable of inducing
apoptosis. May protect cells against TRAIL mediated apoptosis
through ligand competition. Cannot induce the NF-kappa-B pathway.
CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -|- TISSUE SPECIFICITY: Ubiquitous.
CC -|- SIMILARITY: Contains 3 TNFR-Cys repeats.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to licensee@isb-sib.ch).

EMBL; AJ278264; CAC16405.1; +
DR ENBL; AJ276505; CAC27352.1; -
DR ENBL; AY165625; AAN87805.1; -
DR ENBL; AY046550; AAU05072.1; -
DR HSSP; Q9Z9S6; tJM4.
DR MGD; MG1:1930269; Trnfzf23.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.
DR InterPro; IPRO01368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SMO0208; TNFR; 3.
DR PROSITE; PS00652; TNFR NGFR_1; 3.
DR PROSITE; PS00050; TNFR NGFR_2; 2.
KW Glycoprotein; GPI-anchor; Lipoprotein; Receptor; Repeat; Signal.
FT SIGNAL 1 29
FT CHAIN 30 155 Tumor necrosis factor receptor
 superfamily member 23.
FT FT 156 176 Removed in mature form (Potential).
FT LPID 155 155 GPI-anchor amidated cysteine (Potential).
FT REPEAT 37 72 TNFR-Cys 1.
FT REPEAT 74 114 TNFR-Cys 2.
FT REPEAT 115 155 TNFR-Cys 3.
FT DISULFID 38 49 By similarity.
FT DISULFID 50 63 By similarity.
FT FT 53 72 By similarity.
FT DISULFID 75 90 By similarity.
FT DISULFID 93 106 By similarity.
FT DISULFID 96 114 By similarity.
FT DISULFID 116 131 By similarity.
FT DISULFID 134 147 By similarity.
FT DISULFID 137 155 By similarity.
FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 176 AA; 19594 MW; EE30D617F49DDB7D CRC64;

Query Match 68.7%; Score 746.5; DB 1; Length 176;
Best Local Similarity 75.1%; Pred. No. 3.9e-56;
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;

Qy 7 SLVSSLRWFLRRLLLLLLLNLNLPLOYKFAMLEHLHSPCKPAGEYWSKDVCCKNCAG 66
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 5 SHVSLSLHWF-----LLLLLLNFLPLVPAMPESYSFNCPDGYESQNVDVCKTCPGS 56
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Qy 67 TFVKAPCEIPTHQQCQEKCHPGTFTEKDNLYLDACILGSTCDKKDEWADCSATSDRKCQC 126
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Dd 57 TFVKAPCKIPHTQQCQCHKBPPTFGNDGLGHDELCLSTCDKNQMWADCSATSDRKCEC 116
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Qy 127 RTGLYYDPFKFPSCRCCTCRPOGIPIVLQECNSTANTVCSSSVNPNRNRLILLPSLVSL 186
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

KW	Receptor.
357	AA; 40662 MW; 1652B4840D9EEDBA CRC64;
SO	SEQUENCE

```

Query Match      25.8%; Score 280; DB 2; Length 357;
Best Local Similarity 32.4%; Pred. No. 5.8e-16;
Matches 61; Conservative 34; Mismatches 75; Indels 18; Gaps 4;

Oy 20 RLLLLLLLLNL-----PQVKFAMLELHSPKCPAG-EYWSKDVCKKCSA 65
Db 2 RYITLLVLLLNVINAAHSHGLAWHRSVKRL--SRDVSRCRGLEYPHENICLLNCPA 59

Oy 66 GTFVKAPCEIPHTQGCCKHPGTFTEKDNVLDACILCSTCDKQDMVADCSATSDRKQ 125
Db 60 GTYVKKACAAAEKGVCAPCFEFTYTHDHLKLCISCDKCRIDQETIEKTSQNTNRCK 119

Oy 126 CRTGLYYDPKPPESCPRCTKCPGQIPVLQECNSTANTVVC--SSSVNPNRNLFLLSPL 183
Db 120 CRNGSFCLPDQACEVCKKCRCKEDETEKSTAIQNTVCRKRNSPGSSTMTPIVIMPL 179

Oy 184 SVLIVSVV 191
Db 180 IVLLACVL 187

RESULT 9
ID Q6DJ81 PRELIMINARY; PRT; 321 AA.
AC Q6DJ81;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC8957 protein.
GN Name=MGC8957;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Stalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2];
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075302; AAH75302.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR000345; CytC heme BS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.

```

```

DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00198; 4FE4S FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 321 AA; 36225 MW; 21E69219ABB34673 CRC64;

Query Match      24.4%; Score 265.5; DB 2; Length 321;
Best Local Similarity 34.0%; Pred. No. 9.1e-15;
Matches 65; Conservative 25; Mismatches 72; Indels 29; Gaps 5;

Oy 4 FFCSLVSSLSRWFLRRLLLLLLLLLLNLPLQVKFAMLELHSPKCPAGEYWSKDVCKKNC 63
Db 8 FFC-----IFLLAAPITNGLPLS-----SDLY-----YQEGNIRCLRC 40

Oy 64 SAGTFVKAPCEIPHTQGCCKHPG-TFTEKDNVLDACILCSTCDKQDMVADCSATSDR 122
Db 41 PAGTFVEKPCTKPTDIGECSSCHTGSTYSEGTGLDHCLTCLRCRDDQBEVRPCTATQNA 100

Oy 123 KCCRTGLYYDPKPPESCPRCT-KCPQGIPLVQECNSTANTVCCSSSVNPNRNLFLLS 181
Db 101 ECRCKKGTCTPIDHPCVECLTCTCKCPGQELQFPNCNSTSDSCGPAESGSWIVLWLVL 160

Oy 182 PLSVLIVSVV 192
Db 161 PLLLLVLIVV 171

RESULT 10
Oy Q76B99 PRELIMINARY; PRT; 328 AA.
AC Q76B99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Death receptor-M1.
GN Name=xDR-M1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1];
RP SEQUENCE FROM N.A.
RX PubMed=14668340; DOI=10.1074/jbc.M306217200;
RA Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;
RT "Xenopus death receptor-M1 and -M2, new members of the tumor necrosis
RT factor receptor superfamily, trigger apoptotic signaling by
RT differential mechanisms.";
RL J. Biol. Chem. 279:7629-7635(2004).
DR EMBL; AB111446; BAD11770.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4FE4S FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 328 AA; 37252 MW; 444D62A8ACBF9525 CRC64;

```


Db 47 CQEGLYREHLFCQCPPPGKRKNGDCRDRGDMPECVLCSEGNEYTDKSHHSDKCIRCSVC 106

DR InterPro; IPR011029; DEATH_like.

```

QY 107 KDQ--EMVADCSATSDRKCCOCTGLYYDYKPEBESCPCTCKPQIGIPVLQECNSTANTV 164
D 107 DEEHGLEVEHNCRTQNTQCKCKGN-PFCNSPSCPEHCNPCTTCEHGI--IEKPTPTSNYK 163
QY 165 CSSSVSNRNRLFLLLSLPSLVLIYVVVFRIIR 198
D 164 CKGRSH-TNSIALLLILLILLIIFLIYKVVR 196

RESULT 13
Q678B7 PRELIMINARY; PRT; 289 AA.
AC Q678B7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Lymphocystis disease virus - isolate China.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
OX NCBI_TaxID=256729;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
RA Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;
RT "Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
RT China.";
RL J. Virol. 78:6982-6994 (2004).
DR EMBL; AY380826; AAU10940.1; -.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Hypothetical protein.
SQ SEQUENCE 289 AA; 32691 MW; 26B6114DAD5D6C3F CRC64;

Query Match 22.0%; Score 239.5; DB 2; Length 289;
Best Local Similarity 38.7%; Pred. No. 1.4e-12;
Matches 55; Conservative 13; Mismatches 49; Indels 25; Gaps 5;

QY 24 LLLLLLLNPLOVKFAMLELHSPKAGEYMSKDVCKNCNSAGTFVKAPCEIPHTQOCE 83
D 1 MMLFILFLPITVHTAT-----DCPPGYIISKYV-----PAGT-----PMCS 37
QY 84 KCHFGTEKDNLYDACILCSTCDKQDEMVAADCSATSDRKCCOCTGLYYDYKPEBESCRP 143
D 38 PCSFGTYTGLQNSLRKLCRCSTCSHNEPKVACSTTSDVQCQCRQG-YYIDPE-SEMCFF 95
QY 144 CTKCPQIGIPVLQECNSTANTVC 165
D 96 CSNCESSKVKVTCNRTNTHDTC 117

RESULT 14
Q95185 PRELIMINARY; PRT; 189 AA.
AC Q95185;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumour necrosis factor receptor p60 (Fragment).
GN Name=TNFR-1;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX Duthie S., Nasir L., Eckersall P.D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.

```

```

DR HSSP; P19438; IEXT.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF00020; TNFR_c6; 3.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor.
FT NON TER. 189 189
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;

Query Match 22.0%; Score 239; DB 2; Length 189;
Best Local Similarity 35.3%; Pred. No. 1e-12;
Matches 55; Conservative 19; Mismatches 70; Indels 12; Gaps 5;

QY 22 LLLLLLLNPLOVKFAM-----LELHSPKAGEY---WSKDVCKNCNSAGTFVKAPC 73
D 13 LVLLALLVEIYPLRVTLGLVPHLRDRKRAIPCPQGYIHPQDINSICCTCKHGTLYLND 72
QY 74 EIPHTQOCEKCHPGTETKDNLYDACILCSTCDKQ--QEMVADCSATSDRKCCOCTGLY 131
D 73 EGFELDTDCRENGTFTASENYLRQLCSCKRKMVQVEISPTVYRDTVCGCRKNQY 132
QY 132 -YYDPKPEBESCRPCTCKPQIGIPVLQECNSTANTVC 166
D 133 RYVSETHFOCLNSCLNG-TVQISCKETQNTVCT 167

RESULT 15
TNR6_BOVIN STANDARD; PRT; 323 AA.
AC P51867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumour necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95 antigen)
GN Name=TNFRSF6; Synonyms=APT1, FAS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96226401; PubMed=8634151;
RA Yoo J., Stone R.T., Beattie C.W.;
RT "Cloning and characterization of the bovine Fas.";
RL DNA Cell Biol. 15:227-234 (1996).
CC -1- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -1- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: Contains a death domain involved in the binding of FADD,
CC and maybe to other cytosolic adaptor proteins.
CC -1- SIMILARITY: Contains 1 death domain.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```


THIS PAGE BLANK (USPTO)

Result No.	Query			DB	ID	Description	
	Score	Match	Length				
1	702	100.0	702	6	AR403754	AR403754 Sequence	
2	702	100.0	736	6	AV165626	AV165626 Mus musc	
3	602	85.8	691	10	AV165627	AV165627 Mus musc	
4	602	85.8	1550	6	AR403753	AR403753 Sequence	
5	594.4	84.7	1555	6	AY046551	AY046551 Mus musc	
6	578.6	82.4	669	10	MMU278265	AJ278265 Mus musc	
7	511	72.8	1200	6	AR403757	AR403757 Sequence	
8	412	58.7	412	6	AR403752	AR403752 Sequence	
9	377.4	53.8	531	10	AY046550	AY046550 Mus musc	
10	377.4	53.8	569	10	MMU278264	AJ278264 Mus musc	
11	377.4	53.8	1491	10	AV165625	AV165625 Mus musc	
12	377.4	53.8	1509	6	AR164284	AR164284 Sequence	
C	13	136.6	19.5	203141	10	AC068006	AC068006 Mus musc
13	136.6	19.5	281000	10	MMU276505	AJ276505 Mus musc	
15	131.2	18.7	262	6	CQ731135	CQ731135 Sequence	
16	115	16.4	272	6	CQ742972	CQ742972 Sequence	
17	92.8	13.2	240262	2	AC129151	AC129151 Rattus no	
18	87	12.4	2730	5	AB080946	AB080946 Paralict	
19	80.4	11.5	615	6	AY0467100	AY0467100 Sequence	

	Query Match	100.0%;	Score 702;	DB 6;	Length 702;	
	Best Local Similarity	100.0%;	Pred. No. 8e-182;			
	Matches 702;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	TTGCACTCGGCCATGTTTGGCTTCTTCGCAGCTTGCGTGTCCAGTCTGAGTCTGCTGGTTC	60			
DB	1	TTGCACTCGGCCATGTTTGGCTTCTTCGCAGCTTGCGTGTCCAGTCTGAGTCTGCTGGTTC	60			
QY	61	CTTTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGNAATGCGCCTTGCAGGTA	120			
DB	61	CTTTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGNAATGCGCCTTGCAGGTA	120			
QY	121	AAATTGCTATGCTAGAATTACACTCCTTCAAATGTCGGCTGGTGAATACTGGTCTAAA	180			
DB	121	AAATTGCTATGCTAGAAATTACACTCCTTCAAATGTCGGCTGGTGAATACTGGTCTAAA	180			
QY	181	GAGGCTGTGTGAAGNACTGTCTGCAGGTACATTTGTCAAGCGCGCCTCGGAAATCCCC	240			
DB	181	GAGGCTGTGTGAAGAACTGTCTGCAGGTACATTTGTCAAGCGCGCCTCGGAAATCCCC	240			
QY	241	CATACCTCAAGGCAATGTGAGAAGTGTCACCCAGGAACTTTCACAGAGAAGATAAATTAC	300			

```
Db 241 CATACTCAAGACCAATGTGAGAGTGTCCACCAGGAACATTCACAGAGAAAGATAATTAC 300
Qy 301 CTGGATGCTTGTATATTTTGTCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 360
Db 301 CTGGATGCTTGTATATTTTGTCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 360
Qy 361 TCAGCCACAGTACCGGAAATGCCAGTGGCGAAGAGTCTTTTACTATATGACCCAAAA 420
Db 361 TCAGCCACAGTACCGGAAATGCCAGTGGCGAAGAGTCTTTTACTATATGACCCAAAA 420
Qy 421 TTTCAGAAATCGTGGCCCAATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAA 480
Db 421 TTTCAGAAATCGTGGCCCAATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAA 480
Qy 481 TGCAACTCCACAGCTAACACTGTGTGCAAGTTCATCTGTTTCAAGAAGATCTGCCTCAGTG 540
Db 481 TGCAACTCCACAGCTAACACTGTGTGCAAGTTCATCTGTTTCAAGAAGATCTGCCTCAGTG 540
Qy 541 GCCTGGCTATCTGAATGGTTCACAGATCCCAAGAACCGGCTGTCTACTCTATTATCA 600
Db 541 GCCTGGCTATCTGAATGGTTCACAGATCCCAAGAACCGGCTGTCTACTCTATTATCA 600
Qy 601 CCTTTGAGTGTGCTAAATGTGCTGCTGCTCTTCCGTATCATAAAGAAATAAGGTTT 660
Db 601 CCTTTGAGTGTGCTAAATGTGCTGCTGCTCTTCCGTATCATAAAGAAATAAGGTTT 660
Qy 661 TACAGATGTTTCTTAGCTTCTCTTTTATGCTATGAAGTGAT 702
Db 661 TACAGATGTTTCTTAGCTTCTCTTTTATGCTATGAAGTGAT 702
```

RESULT 2
AY165626
LOCUS
DEFINITION Mus musculus decoy TRAIL receptor 2 short form (Dctrailr2) mRNA,
complete cds; alternatively spliced.

ACCESSION
VERSION
KEYWORDS
SOURCE
AY165626.1 GI:27985789

ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 736)
Schneider,P., Olson,D., Tardivel,A., Browning,B., Lugovskoy,A.,
Gong,D., Dobles,M., Hertig,S., Hofmann,K., Van Vlijmen,H.,
Heu,Y.-M., Burkly,L., Tschopp,J. and Zheng,T.S.
Identification of a New Murine Tumor Necrosis Factor Receptor Locus
That Contains Two Novel Murine Receptors for Tumor Necrosis
Factor-related Apoptosis-inducing Ligand (TRAIL)
J. Biol. Chem. 278 (7), 5444-5454 (2003)

JOURNAL
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 736)
Schneider,P., Olson,D., Tardivel,A., Browning,B., Lugovskoy,A.,
Gong,D., Dobles,M., Hertig,S., Hofmann,K., Van Vlijmen,H.,
Heu,Y.-M., Burkly,L., Tschopp,J. and Zheng,T.S.
Direct Submission
Submitted (16-OCT-2002) Institute of Biochemistry, University of
Lausanne, Boveresses 155, Epalinges CH-1066, Switzerland
Location/Qualifiers

FEATURES
source
1..736
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/chromosome="7"
1..736
/gene="Dctrailr2"
/note="synonym: Tnfrh2"
31..573
/gene="Dctrailr2"
/note="mDctrailr2S; binds both murine and human TRAIL;

secreted soluble form; member of the TNFR family;
alternatively spliced
/codon_start=1
/product="decoy TRAIL receptor 2 short form"
/protein_id="AA87806.1"
/db_xref="GI:27985790"
/translation="MFGPFCSLVSSLSRWFLWRLLLLLLLLLLLNPLOVKFAMLELH
SFKCPAGEYWSKDVCKKNSAGTVPKAPCEIPIHTQCEKCHGFTFEKKNYLDACLIL
CSTCDKQEMVADCSATSDRKQCTGLYYIDPKFPESCRPCTKCPQIPLQBCNST
ANTVCSSSVSRSSAVAWPI"

ORIGIN

Query Match 100.0%; Score 702; DB 10; Length 736;
Best Local Similarity 100.0%; Pred. No. 8e-182; Indels 0; Gaps 0;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTGCACCTCGGCCCATGTTTGGCTTCTTCTGCAGCTTGGTCTCCAGTCTGAGTCTGCTGCTTC 60
Db 19 TTGCACCTCGGCCCATGTTTGGCTTCTTCTGCAGCTTGGTCTCCAGTCTGAGTCTGCTGCTTC 78
Qy 61 CTTTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 79 CTTTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 138
Qy 121 AAATTTGCTATGCTAGAAATTACACTCCTTCAAAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 139 AAATTTGCTATGCTAGAAATTACACTCCTTCAAAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 198
Qy 181 GAGCTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCGAAGCGCCCTCGAAATCCCC 240
Db 199 GAGCTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCGAAGCGCCCTCGAAATCCCC 258
Qy 241 CATACTCAAGGACAAATGTGAGAAAGTGTACCCAGGAACATTCACAGAGAAAGATAATTAC 300
Db 259 CATACTCAAGGACAAATGTGAGAAAGTGTACCCAGGAACATTCACAGAGAAAGATAATTAC 318
Qy 301 CTGGATGCTTGTATATTTTGTCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 360
Db 319 CTGGATGCTTGTATATTTTGTCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 378
Qy 361 TCAGCCACAGTACCGGAAATGCCAGTGGCCGAAACCGGCTGTCTTACTACTATGACCCAAAA 420
Db 379 TCAGCCACAGTACCGGAAATGCCAGTGGCCGAAACCGGCTGTCTTACTACTATGACCCAAAA 438
Qy 421 TTTCCAGAAATCGTGGCCGCCCATGTATCAAGTGTCCCCCAAGGAATCCCTGTCTCCAGGAA 480
Db 439 TTTCCAGAAATCGTGGCCGCCCATGTATCAAGTGTCCCCCAAGGAATCCCTGTCTCCAGGAA 498
Qy 481 TGCAACTCCACAGCTAACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 499 TGCAACTCCACAGCTAACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 558
Qy 541 GCCTGGCTATCTGAATGGTTCACAGATCCCAAGAACCGGCTGTCTTACTACTATGATATCA 600
Db 559 GCCTGGCTATCTGAATGGTTCACAGATCCCAAGAACCGGCTGTCTTACTACTATGATATCA 618
Qy 601 CTTTGAAGTGTGCTAAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 619 CTTTGAAGTGTGCTAAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
Qy 661 TACAGATGTTTCTTAGCTTCTCTTTTATGCTATGAAGTGAT 702
Db 679 TACAGATGTTTCTTAGCTTCTCTTTTATGCTATGAAGTGAT 720

RESULT 3
AY165627
LOCUS
DEFINITION Mus musculus decoy TRAIL receptor 2 long form (Dctrailr2) mRNA,
complete cds; alternatively spliced.
ACCESSION
VERSION
KEYWORDS
AY165627.1 GI:27986023


```

Qy 361 TCAGCCACGAGTACCGGAATGCCAGTGCAGAACAGGCTCTTTACTATGACCCAAA 420
Db 361 TCAGCCACGAGTACCGGAATGCCAGTGCAGAACAGGCTCTTTACTATGACCCAAA 420
Qy 421 TTTCCAGAACTCGTCCGCCCATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGAA 480
Db 421 TTTCCAGAACTCGTCCGCCCATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGAA 480
Qy 481 TGCAACTCCACAGCTAACACCTGTGTGAGTTCATCTGTTCCTCAAGAAATCTGCTCAGTG 540
Db 481 TGCAACTCCACAGCTAACACCTGTGTGAGTTCATCTGTTCCTCAAGAAATCTGCTCAGTG 540
Qy 541 GCCTGGCCCTATCTGAATGTTTCACAGAGATCCCAAGAAACCGGCTGTTCCTACTATCA 600
Db 541 GCCTGGCCCTATCTGAATGTTTCACAGAGATCCCAAGAAACCGGCTGTTCCTACTATCA 600
Qy 601 CCTTTGAGTGTGCTAAATGTGCTCGTGTGCTGCTTCCGTATCATCAAGAAATGAGGTTTC 660
Db 601 CCTTTGAGTGTGCTAAATGTGCTCGTGTGCTGCTTCCGTATCATCAAGAAATGAGGTTTC 660
Qy 661 TACAGATGTTTCTTAGCTTCTCTTTTATGCTATCAAGTGTAT 702
Db 661 TACAGATGTTTCTTAGCTTCTCTTTTATGCTATCAAGTGTAT 702

RESULT 5
AY046551 1555 bp mRNA linear ROD 03-JAN-2002
LOCUS Mus musculus TNF receptor family member SOBA mRNA, complete cds.
ACCESSION AY046551
VERSION AY046551.1 GI:18056435
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1555)
AUTHORS Ribser, P., Mao, W., Baldwin, D. and Pan, G.
TITLE Characterization of SOBA, a murine member of the TNFR family
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1555)
Pan, G. and Baldwin, D.
DIRECT SUBMISSION
TITLE Submitted (18-JUL-2001) Molecular Oncology, Genentech, Inc, 1 DNA
JOURNAL Way, South San Francisco, CA 94080, USA
FEATURES
source
1..1555
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
7..603
/codon_start=1
/product="TNF receptor family member SOBA"
/protein_id="AA05073.1"
/db_xref="GI:18056436"
/translaton="MFQGFCSLVSSVSFRWFLRRLLLLLLLLPQVFKAMLEIH
SFKCPAGEYWSKDCCKNKGAFVKAPEIPIHQGCEKHPGTFFKKNYLDACIL
CSTCKDQEMVADCSATSDRKCQCRGTGLYYDKFEPSCRPCTKCPQGIPIVQBCNST
ANTVCSSSVNPRNRLFLLSPLSVLVSVVFIIR"

CDS
84.7%; Score 594.4; DB 10; Length 1555;
Best Local Similarity 93.4%; Pred. No. 3.2e-152;
Matches 650; Conservative 0; Mismatches 1; Indels 45; Gaps 1;

Qy 7 TCGGCCATGTTGGCTTCTTCGAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 66
Db 7 TCGGCCATGTTGGCTTCTTCGAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 66
Qy 67 CGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126
Db 67 CGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126

```

```

Qy 127 GCTATGCTAGAAATTAACAATGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186
Db 127 GCTATGCTAGAAATTAACAATGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Qy 187 TGTTCAGAACTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246
Db 187 TGTTCAGAACTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 247 CAAGGACAAATGCTGAGAAATGCTCAACCCAGGAACATTCACAGAGAAAGATAATATACCTGGAT 306
Db 247 CAAGGACAAATGCTGAGAAATGCTCAACCCAGGAACATTCACAGAGAAAGATAATATACCTGGAT 300
Qy 307 GCTTGTATATCTTGTCTCCACCTGTGATAAAGATCAGAAATGCTGCGCAGATGCTGCTCAGCC 366
Db 307 GCTTGTATATCTTGTCTCCACCTGTGATAAAGATCAGAAATGCTGCGCAGATGCTGCTCAGCC 360
Qy 367 ACCAGTGACCGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
Db 367 ACCAGTGACCGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 427 GAATCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
Db 427 GAATCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 487 TCACAGCTAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
Db 487 TCACAGCTAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 517
Qy 547 CCTATCTGAATGCTTACAGAGATCCAGAAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
Db 547 CCTATCTGAATGCTTACAGAGATCCAGAAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
Qy 558 -----ATCCAGAAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
Db 558 -----ATCCAGAAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
Qy 607 AGTGTGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
Db 607 AGTGTGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
Qy 667 TGTTCCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
Db 667 TGTTCCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651

```

RESULT 6

```

MMU278265 669 bp mRNA linear ROD 06-MAR-2002
LOCUS Mus musculus domesticus mRNA for tumor necrosis factor receptor p60
DEFINITION homologue 2 (Tnfrh2 gene).

```

```

ACCESSION AJ278265
VERSION AJ278265.1 GI:11191811

```

```

KEYWORDS Tnfrh2 gene; tumor necrosis factor receptor p60 homologue 2.
SOURCE Mus musculus domesticus (western European house mouse)

```

ORGANISM

```

Mus musculus domesticus
Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE

```

1 Engemann, S., Strodick, M., Paulsen, M., Franck, O., Reinhardt, R.,
Lane, N., Reik, N. and Walter, J.

```

```

Sequence and functional comparison in the Beckwith-Wiedemann
region: implications for a novel imprinting centre and extended

```

```

imprinting
Hum. Mol. Genet. 9 (18), 2691-2706 (2000)

```

JOURNAL

```

MEDLINE 20519229
PUBMED 11063728

```

REFERENCE

```

2 (bases 1 to 669)

```

AUTHORS

```

Engemann, S.

```

TITLE

```

Submitted (30-MAY-2000) Engemann S., Department Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195

```

JOURNAL

```

Berlin, GERMANY

```

FEATURES

```

source
1..669
/organism="Mus musculus domesticus"
/mol_type="mRNA"

```


	/sub_species="domesticus" /db_xref="taxon:10092" /chromosome="7" 1..669 /gene="Tnfrh2" 83..508 /gene="Tnfrh2" /codon_start=1 /evidence=experimental /product="tumor necrosis factor receptor p60 homologue 2" /protein_id="CAC16406.1" /db_xref="GI:11191812" /db_xref="GOA:Q9ER62" /db_xref="UniProt/Swiss-Prot:Q9ER62" /translation="MELHSFKPAGBYNSKDCCKNCSAGTSFVKAPCEIPHPTQGQCE KCHPGTPTEKDNTLDILICSTCDKQEMVADCSATSDRKQCQRCTGLYYVDPKFPESC RPCTKCPQGIPLVLQECNSTANTVCSSSVSRSSASVAWPI"
gene	
CDS	
ORIGIN	
Query Match	82.4%; Score 578.6; DB 10; Length 669;
Best Local Similarity	97.3%; Pred. No. 6.9e-148;
Matches 640; Conservative	0; Mismatches 12; Indels 6; Gaps 5;
QY	46 CTGAGTCGTGGTTCCITTCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAAT 105 DB 1 CTGAGTCGTGGTTCCITTCGGCGGCGCTGCTGCTG--TGCTGNTGNTGTG--TTGTTAAT 57
QY	106 CTGCCCTTCGAGGTAAATAATT-GCTATGCTAGAATAACACTCCTTCAAAATGTCCTCCGCTGG 164
DB	58 CTGCCCTTCGAGGTAAATAATTGGCTATGCTAGAAATACACTCCTTCAAAATGTCCTCCGCTGG 117
QY	165 TGAATACGTGCTAAAGACGCTCTGTTGCAGAGAACGTGTTCTGCAGGTACATTTGTCAAGGC 224
DB	118 TGAATACGTGCTAAAGACGCTGTTTGCAGAGAACGTGTTCTGCAGGTACATTTGTCAAGGC 177
QY	225 GCCTTGCGAAATCCCCATACCTAAGACAATGTGAGAAGTGTACCACCGAGAACATTTCAC 284
DB	178 GCCTTGCGAAATCCCCATACCTAAGACAATGTGAGAAGTGTACCACCGAGAACATTTCAC 237
QY	285 AGAGAAAGATAAATTTACCTGGATGCTTGTATATCTTTGCTCCACCTGTGATAAAAGATCAGGA 344
DB	238 AGAGAAAGATAAATTTACCTGGATGCTTGTATATCTTTGCTCCACCTGTGATAAAAGATCAGGA 297
QY	345 AATGGTGGCCGACTGCTCAGCCACAGTGACCGGAAATGCCAGTGC CGAAGCATGCTTTTA 404
DB	298 AATGGTGGCCGACTGCTCAGCCACAGTGACCGGAAATGCCAGTGC CGAAGCATGCTTTTA 357
QY	405 CTAATATGACCCAAAAATTTCCAGAAATCGTGGCGGCCCATGTACCAAGTGTGTCCTCCCAAGAAAT 464
DB	358 CTAATATGACCCAAAAATTTCCAGAAATCGTGGCGGCCCATGTACCAAGTGTGTCCTCCCAAGAAAT 417
QY	465 CCCTGTCTCCAGGAATGCAACTCCACAGCTACACGTGTGCGAGTTCATCTGTTTCCAAG 524
DB	418 CCCTGTCTCCAGGAATGCAACTCCACAGCTACACGTGTGCGAGTTCATCTGTTTCCAAG 477
QY	525 AAGATCTGCTCAGTGGCCCTATCTGAATGGTTTACAGAGATCCCAGAAACCGGCT 584
DB	478 AAGATCTGCTCAGTGGCCCTATCTGAATGGTTTACAGAGATCCCAGAAACCGGCT 537
QY	585 GTTCCTACTGTTATCACCTTTGAGTGTGCTAAATTTGTGCCGTTGTTGCTTCGATCAT 644
DB	538 GGTCCTACTGTTATCACCTTTGAGTGTGCTAAATTTGTGCCG-TGGTGGCCTCCGATCAT 596
QY	645 AAGAGATAAAGGTTCTACAGATGTTTTCTTAGCTTCTTTTATGCTATGAAGTGT 702
DB	597 AAGAAGATAAAGG-TCTACAGATGTTTTCTTANCTTCTTTTATTTGCTATGAAGTGT 653
RESULT 7	
AR403757	LOCUS 1200 bp DNA linear PAT 18-DEC-2003
SEQUENCE	Sequence 13 from patent US 6627199.
DEFINITION	AR403757
ACCESSION	AR403757

CDS	AUTHORS	TITLE	JOURNAL	FEATURES
/gene="Tnfrhl" 79..522 /gene="Tnfrhl" /codon_start=1 /evidence=experimental /product="tumor necrosis factor receptor p60 homologue 1" /protein_id="CAC18405.1" /db_xref="GI:11191810" /db_xref="GOA:Q9ER63" /db_xref="UniProt/Swiss-Prot:Q9ER63" translation="WPBESVFNCPDGEYSDNVCCKPSTGFKVKAPKIPHTQGCE KCHPGTFNGKGLHDCLESCDKXNDWADCSATDRKCECOIGLYYYDPKPESP RPTCKPOGIPVLQCNSTANTVCSSSVSNPNLFLMLLVFCI"	Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M., Burkly L., Teschopp J. and Zheng T.S. Submitted (16-OCT-2002) Institute of Biochemistry, University of Lausanne, Boveresses 155, Epalinges CH-1066, Switzerland	Direct Submission	Submitted (16-OCT-2002)	Location/Qualifiers source 1..1491 /organism="Mus musculus" /mol_type="mRNA" /strains="C57BL" /db_xref="taxon:10090" /chromosome="7" 1..1491 /gene="Dctrailr1" /note="synonym: Tnfrh1" 7..537 /gene="Dctrailr1" /note="mDctrailr1"; binds murine TRAIL but not human TRAIL; contains a glycosyl-phosphatidylinositol (GPI) anchor; member of the TNFR family" /codon_start=1 /product="decoy TRAIL receptor 1" /protein_id="AA87805.1" /db_xref="GI:27985588" translation="MVTPSHSVSSLSHWFLLLLNLFPLVFAMPESYSFNCPPGEY SDNVCKTCPSGTFFVKAPKIPHTQGCEKCHPGTFNGKGLHDCLESCDKXNDW VADCSATDRKCECOIGLYYYDPKPESP RPTCKPOGIPVLQCNSTANTVCSSSVS NPRLWLFLMLLVFCI"
ORIGIN	Query Match Best Local Similarity Matches	Score 377.4; DB 10; Length 569; 90.7%; Pred. No. 1.5e-92; Conservative 0; Mismatches 41; Indels 0; Gaps 0;		
QY	81	GCTGCTGCTGCTGCTGCTGAATCTGCCCTGGAGTAATCTGGTCTTAAAGACACTGCTTCAAGAACCTG 200		
Db	30	GTTCCCTCTTGCTGCTGCTGAATCTGTTCTTGCCTGTAATAATTGCTATGCTGAATC 89		
QY	141	ACACTCTTCAAATGTCCTCGCTGGTGAATCTGCTTAAAGACACTGCTTCAAGAACCTG 200		
Db	90	ATACTCTTCAAATGTCCTCGCTGGTGAATCAACCAGTCTAATGATGCTGTTGCAAGACCTG 149		
QY	201	TTCCTGAGGTACATTTGTCAGGCGCTCGCAATCCCCCATCTCAAGACCAATGTGA 260		
Db	150	TCCTCAGGTACATTTGTCAGGCGCTCGCAATCCCCCATCTCAAGACCAATGTGA 209		
QY	261	GAAGTGTCAACCCAGGAACAATTCACAGAGAAGATAATTAACCTGGATGCTTGTATATTG 320		
Db	210	GAAGTGTCAACCCAGGAACAATTCACAGGGAAGATAATGCGCTGCATGATTTGTGAATTTG 269		
QY	321	CTCCACCTGTGATAAGACCAAGCAATTCACAGGCAATGCTGCTGAGGCACTGACCCGAA 380		
Db	270	CTCCACCTGTGATAAGACCAAGCAATTCACAGGCAATGCTGCTGAGGCACTGACCCGAA 329		
QY	381	ATGCCAGTCCGAAACAGGTCTTTACTATATACCAACAAAATTTCCAGAACTGTCGCCGCC 440		
Db	330	ATGCCAGTCCGAAACAGGTCTTTACTATATACCAACAAAATTTCCAGAACTGTCGCCGCC 389		
QY	441	ATGTACCAAGTGTCCCAGGAATCCCTGCTCCAGGAATGCAACTCCACAGCTAACAC 500		
Db	390	ATGTACCAAGTGTCCCAGGAATCCCTGCTCCAGGAATGCAACTCCACAGCTAACAC 449		
QY	501	TGTTGTCAGTTTCATCTGTTTTCAA 523		
Db	450	TGTTGTCAGTTTCATCTGTTTTCAA 472		
RESULT 11	AY165625	1491 bp mRNA linear ROD 19-FEB-2003		
LOCUS	Mus musculus			
DEFINITION	Mus musculus decoy TRAIL receptor 1 (Dctrailr1) mRNA, complete cds.			
ACCESSION	AY165625			
VERSION	AY165625.1 GI:27985587			
KEYWORDS	Mus musculus (house mouse)			
SOURCE	Mus musculus			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 1491) Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M., Burkly L., Teschopp J. and Zheng T.S.			
AUTHORS	Identification of a New Murine Tumor Necrosis Factor Receptor Locus That Contains Two Novel Murine Receptors for Tumor Necrosis Factor-related Apoptosis-inducing Ligand (TRAIL)			
TITLE	J. Biol. Chem. 278 (7), 5444-5454 (2003)			
JOURNAL	PUBLISHED	12466268		
REFERENCE	2 (bases 1 to 1491)			
LOCUS	AR164284	1509 bp DNA linear PAT 17-OCT-2003		
DEFINITION	Sequence 3 from patent US 6271366.			
ACCESSION	AR164284			

region: implications for a novel imprinting centre and extended imprinting
Hum. Mol. Genet. 9 (18), 2691-2706 (2000)
20519229
11063728
REFERENCE
AUTHORS
TITLE
JOURNAL
Engemann, S.
Direct Submission
Submitted (17-MAR-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GERMANY
Revised by author 22-MAY-2000
3 (bases 1 to 281000)
Engemann, S.
Direct Submission
Submitted (22-NOV-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GERMANY
4 (bases 1 to 281000)
Engemann, S.
Direct Submission
Submitted (24-JAN-2001) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GERMANY
COMMENT
On Jan 27, 2001 this sequence version replaced gi:1191799.
related accession numbers AJ300452-AJ300460
has a 1000 bp overlap with AJ271885.
FEATURES
source
1. 281000
/organism="Mus musculus domesticus"
/mol_type="genomic DNA"
/strain="129 SV"
/sub_species="domesticus"
/db_xref="taxon:10092"
/chromosome="7"
/cell_line="CJ7"
1431..28364
/gene="Obph1"
join(<1431..1455,3536..3622,7265..7345,7478..7578,
7906..8110,9688..9772,11978..12149,12416..12608,
13783..13967,14347..14428,15828..15926,16308..16404,
17790..17888,21514..21610,21996..22086,22181..22317,
22743..22928,23228..23354,24142..24268,25136..25238,
27169..28364)
/gene="Obph1"
join(1432..1455,3536..3622,7265..7345,7478..7578,
7906..8110,9688..9772,11978..12149,12416..12608,
13783..13967,14347..14428,15828..15926,16308..16404,
17790..17888,21514..21610,21996..22086,22181..22317,
22743..22928,23228..23354,24142..24268,25136..25238,
27169..27307)
/gene="Obph1"
/codon_start=1
/product="oxysterol binding protein"
/protein_id="CAC27351.1"
/db_xref="GI:12583596"
/db_xref="GOA:Q9ER64"
/db_xref="UniProt/Swiss-Prot:Q9ER64"
/translation="MSLVPSQPGRDMESNGSPQDRBEPOTPGSATKVPVLAERYLCN
GSDKECPPTFVSKDALKAKENYRQEKKATKQFSAITDPSVIMADSLKIGCT
LKSWTKLKCVLKPQVLLIYKTPYKGVQWGTVLLHCCBLIERPSKQGFCKLFPPLDQ
SWAVKPGKSGSITQPLPSSYLI1FRAASESDRCWLDALALRCSSLLRLSTCK
QGRDEQSSPDSPSSLYGLPTSATIPDQDLFPNGSALENDAFSDKSERENABSD
AETQDHRKNTSGSDLLDSPGPGWGTYYVQVEQELGELDETSQVETVSEENKSLM
WLLRLRPGMDLSRVLPVFLVPRSFGLKSLDYHHGDLSSRAAEADDPYKCMKLV
LRWLSGFYKPKGKKPYNPILGETFRCWLHPQTSHTFVIAEVSHPHPYSAFV
SNRKDGFCSGSITAKSKFYNGSNSALLDKAKLITFLNRKEEYTLTPYAHRCGILIG
TLMELGKVNIECKNNQAEFLKLPFGSSANINISGKIMSGEEVLVRLTGHW
DRDVFIEESGGTFLFWPSEEVRRQLRKHTVLLLEEQSELERLQHWVTRAIRG
DQHKATQKRLVLEAQRARHQQSITPMKPOLFLDPLTQEWRYRYEDLSWPDPLK
DIAQYEDGILHTMSQQTFLGSDSRHKRPPSSDRLRKASQPSGSHSVTES
SGSTPSCPDLSDEDVFPDGGSPGCRREVRHLKMLQEAFLSIQEAQELHRLHSTM
LSSVTRAGQAAPALLQNPRSWFLICLTLCQLFINTLK"

exon
1432..1455
/gene="Obph1"
/number=1
3536..3622
/gene="Obph1"
/number=2
7265..7345
/gene="Obph1"
/number=3
7478..7578
/gene="Obph1"
/number=4
7906..8110
/gene="Obph1"
/number=5
9688..9772
/gene="Obph1"
/number=6
11978..12149
/gene="Obph1"
/number=7
12416..12608
/gene="Obph1"
/number=8
13783..13967
/gene="Obph1"
/number=9
14347..14428
/gene="Obph1"
/number=10
15828..15926
/gene="Obph1"
/number=11
16308..16404
/gene="Obph1"
/number=12
17790..17888
/gene="Obph1"
/number=13
21514..21610
/gene="Obph1"
/number=14
21996..22086
/gene="Obph1"
/number=15
22181..22317
/gene="Obph1"
/number=16
22743..22928
/gene="Obph1"
/number=17
23228..23354
/gene="Obph1"
/number=18
24142..24268
/gene="Obph1"
/number=19
25136..25238
/gene="Obph1"
/number=20
27169..27307
/gene="Obph1"
/number=21
join(30593..130688,131306..131403,132305..132456,
140377..140517,141097..141184,142468..142590,
145511..145624,146438..146565,146958..147085,
147169..147274,147610..147707,147985..148174,
148724..148792,152041..152121,154073..154154,
155189..155255,157406..157466,157904..157988,
159108..159408)
/gene="Cars"
30593..130688
/gene="Cars"
exon
gene

```

/number=5
join(31277..31342,35572..35662,37049..37176,46179..46291,
47068..47141,48531..48627)
/gene="Tnfrh1"
mRNA
join(<31277..31342,35572..35662,37049..37176,46179..46291,
47068..47141,48531..48627)
/gene="Tnfrh1"
CDS
join(35584..35662,37049..37176,46179..46291,47068..47141,
48531..48580)
/gene="Tnfrh1"
/codon_start=1
/product=tumor necrosis factor receptor p60 homologue"
/protein_id="CAC27352.1"
/db_xref="GI:12583597"
/db_xref="GOA:Q9ER63"
/db_xref="UniProt/Swiss-Prot:Q9ER63"
/translators="MPBSYFNPDPGEYQSDVCCCKTSPSGTFVKAPCKIPHTQGOCE
KCHPCTGTGDKGLHDCLELCTCDKQNMVADCSATSDRKECQIGLYYYDPKPFESC
RPTKCPQGPVVLQECNSTANTVCCSSSVSNPRNWLFLMLIVFCI"
35584..35662
/gene="Tnfrh1"
/number=1
37049..37176
/gene="Tnfrh1"
/number=2
46179..46291
/gene="Tnfrh1"
/number=3
47068..47141
/gene="Tnfrh1"
/number=4
48531..48580
/gene="Tnfrh1"
/number=5
join(67525..67596,72244..72334,73711..73838,76251..76363,
77140..77213,77826..77868,78677..78828)
Query Match 19.5%; Score 136.6; DB 10; Length 281000;
Best Local Similarity 94.0%; Pred. No. 2.8e-26;
Matches 142; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 198 GTGTTCTGCGAGTACATTTGTCAAGGGCCCTGCGAAATCCCCATACCTCAAGGACAATG 257
Db 73700 CTTATCCCGAGGTACATTTGTCAAGGGCCCTGCGAAATCCCCATACCTCAAGGACAATG 73759
Qy 258 TGAGAAGTGTCAAGGACAATTTACAGAGAAAGATAATTACCTGGATGCTGTGTACT 317
Db 73760 TGAGAAGTGTCAAGGACAATTTACAGAGAAAGATAATTACCTGGATGCTGTGTACT 73819
Qy 318 TTGCTCCACCTGTGATAAAGATCAGGAAATG 348
Db 73820 TTGCTCCACCTGTGATAAAGGTGATGTG 73850
```

```

RESULT 15
CQ731135
LOCUS CQ731135 262 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 17069 from Patent WO02068579.
ACCESSION CQ731135
VERSION CQ731135.1 GI:42306906
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 17069 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
```

```

source 1..262
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 18.7%; Score 131.2; DB 6; Length 262;
Best Local Similarity 75.2%; Pred. No. 7.4e-25;
Matches 197; Conservative 0; Mismatches 23; Indels 42; Gaps 1;
Qy 118 GTAAAAATTTGCTATGCTAGAAATTACACTCCTTCAAAATGTCCCGCTGGTGAATACTGGTCT 177
Db 1 GTAAATTTTGTCTATGCTGCTGAATCATCTCTTCAACTGTCTCCGATGGTGAATACCACTCT 60
Qy 178 AAAGACGTCTGTTGCAAGAACTGTTCTGCA-----
Db 61 AATGATGTCTGTTGCAAGACCTGTCCCTCAGGTGAGTTCTTCAATGAGACCCAGTGCCAC 120
Qy 208 -----GGTACATTTGTCAAGGGCCCTGCGAAATCCCCATACCTCAAGGACAA 255
Db 121 AGCATAGACATGGGTACATTTGTCAAGGGCCCTGCGAAATCCCCATACCTCAAGGACAA 180
Qy 256 TGTGAGAAGTGTCAAGGACAATTTACAGAGAAAGATAATTACCTGGATGCTGTGTATA 315
Db 181 TGTGAGAAGTGTCAAGGACAATTTACAGAGAAAGATAATTACCTGGATGCTGTGTATA 315
Qy 316 CTTTGTCTCCACCTGTGATAAAG 337
Db 241 CTTTGTCTCCACCTGTGATAAAG 262
```

Search completed: September 8, 2005, 23:31:27
Job time : 7219.45 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 15:59:37 ; Search time 352.87 Seconds
(without alignments)
3255.208 Million cell updates/

Title: US-10-622-407-9

Perfect score:

Sequence: 1 ttgcactcggccatgtttgg.....ttttattgctatgaagtgat 702

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

FOBC-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

```
1: /cn2_6/ptodata/1/lna/5A_COMB.seq.*
2: /cn2_6/ptodata/1/lna/5B_COMB.seq.*
3: /cn2_6/ptodata/1/lna/6A_COMB.seq.*
4: /cn2_6/ptodata/1/lna/6B_COMB.seq.*
5: /cn2_6/ptodata/1/lna/PCRTUS_COMB.seq.*
6: /cn2_6/ptodata/1/lna/backfiles1.seq.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	702	100.0	702	4	US-09-612-033B-7		Sequence 9, Appli
2	602	85.8	1550	4	US-09-612-033B-9		Sequence 7, Appli
3	511	72.8	1200	4	US-09-612-033B-13		Sequence 13, Appl
4	412	58.7	412	4	US-09-612-033B-5		Sequence 5, Appli
5	377.4	53.8	1509	3	US-09-411-723-3		Sequence 3, Appli
6	377.4	53.8	1509	4	US-09-855-266A-3		Sequence 3, Appli
C 7	48.8	7.0	325	2	US-08-531-927B-3		Sequence 3, Appli
	47.6	6.8	1776	2	US-08-531-927B-1		Sequence 1, Appli
C 8	47.6	6.8	1776	3	US-09-041-886-12		Sequence 12, Appl
C 9	47.6	6.8	2224	4	US-09-922-364A-44		Sequence 44, Appl
C 10	47.6	6.8	2224	4	US-09-254-590-44		Sequence 44, Appl
C 11	47.6	6.8	2224	4	US-10-115-415-44		Sequence 44, Appl
C 12	47.6	6.8	2224	4	US-10-115-415-44		Sequence 44, Appl
C 13	47.6	6.8	2224	4	US-10-116-260-44		Sequence 44, Appl
C 14	47.6	6.8	2224	4	US-10-115-671-44		Sequence 44, Appl
C 15	47.6	6.8	2462	4	US-09-922-364A-48		Sequence 48, Appl
C 16	47.6	6.8	2462	4	US-09-254-590-48		Sequence 48, Appl
C 17	47.6	6.8	2462	4	US-10-115-415-48		Sequence 48, Appl
C 18	47.6	6.8	2462	4	US-10-116-260-48		Sequence 48, Appl
C 19	47.6	6.8	2462	4	US-10-115-671-48		Sequence 48, Appl
C 20	47.2	6.7	397	3	US-09-253-691-3		Sequence 3, Appli
C 21	47.2	6.7	601	4	US-09-949-016-44973		Sequence 44973, A
C 22	47.2	6.7	601	4	US-09-949-016-44974		Sequence 44974, A
C 23	47.2	6.7	2514	4	US-09-949-016-1290		Sequence 1290, Ap
C 24	47.2	6.7	15651	4	US-09-949-016-13032		Sequence 13032, A
C 25	46	6.6	3302	4	US-09-620-312D-475		Sequence 475, App
C 26	45.4	6.5	688	3	US-08-998-416-915		Sequence 915, App
C 27	45	6.4	530	4	US-09-640-211A-62		Sequence 62, Appl

C 28	45	6.4	5082	4	US-09-497-822C-18	Sequence 18, Appl
C 29	44.8	6.4	228	6	5273901-10	Patent No. 5273901
C 30	44.8	6.4	228	6	5482709-9	Patent No. 5482709
C 31	44.8	6.4	228	6	5273901-10	Patent No. 5273901
C 32	44.8	6.4	228	6	5482709-9	Patent No. 5482709
C 33	44.8	6.4	4262	4	US-09-521-511C-10	Sequence 10, Appl
C 34	44.6	6.4	4263	4	US-08-997-685A-1	Sequence 1, Appl
C 35	44	6.3	2521	3	US-09-115-446-1	Sequence 1, Appl
C 36	44	6.3	2521	4	US-09-565-590-1	Sequence 1, Appl
C 37	44	6.3	2526	3	US-09-115-446-5	Sequence 5, Appl
C 38	44	6.3	2526	4	US-08-585-590-5	Sequence 5, Appl
C 39	44	6.3	10348	2	US-08-487-273B-41	Sequence 41, Appl
C 40	44	6.3	10348	3	US-08-586-419-13	Sequence 13, Appl
C 41	44	6.3	10348	3	US-09-041-886-14	Sequence 14, Appl
C 42	44	6.3	10366	1	US-08-246-982A-5	Sequence 5, Appl
C 43	44	6.3	10366	1	US-08-453-265-5	Sequence 5, Appl
C 44	43.6	6.2	477	3	US-09-135-994-1	Sequence 1, Appl
C 45	43.6	6.2	477	4	US-09-684-843A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

```

US-09-612-033B-9
; Sequence 9, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Savis, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; Tmat2, a No. 6627199el Member of the TNF-Receptor Superfamily
; TITLE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(552)
; OTHER INFORMATION: Primer 2086-39
US-09-612-033B-9

```

Query Match	100.0%;	Score 702;	DB 4;	Length 702;
Best Local Similarity	100.0%;	Pred. No. 7,7e-215;		
Matches 702;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TTGCACTCGGCCATGTTTGGCTTCTTCTGCAGCTTGGTGTCACGTCTGCAGTCGCTGGTTC	60	
Db	1	TTGCACCTCGGCCCATGTTTGGCTTCTTCTGCAGCTTGGTGTCACGTCTGCAGTCGCTGGTTC	60	
Qy	61	CTTTGGCGGGCGTCTGCTGCTGCTGCTGCTGCTGTAATCTGCCCTTCACAGTA	120	
Db	61	CTTTGGCGGGCGGTCTGCTGCTGCTGCTGCTGCTGTAATCTGCCCTTCACAGTA	120	
Qy	121	AAATTTGCTATGCTAGAAATTACACTCTTCAAATGTCCCGTGGTGAATACTGGTCTAAA	180	
Db	121	AAATTTGCTATGCTAGAAATTACACTCTTCAAATGTCCCGTGGTGAATACTGGTCTAAA	180	
Qy	181	GACGTCGTGTGCAAGAACTGTTCTGCAGGTACATTTGTCGAAGCGCCCTCGGAAATCCCC	240	
Db	181	GACGTCGTGTGCAAGAACTGTTCTGCAGGTACATTTGTCGAAGCGCCCTCGGAAATCCCC	240	
Qy	241	CATACCTCAAGGACAAATGTGAGAGTGTACCCGAGAACATTTCACAGAGAAGATAAATTAC	300	
Db	241	CATACCTCAAGGACAAATGTGAGAGTGTACCCGAGAACATTTCACAGAGAAGATAAATTAC	300	

		85.8%; Score 602; DB 4; Length 1550;
	Best Local Similarity	93.6%; Pred. No. 1.6e-182;
Matches	657; Conservative	0; Mismatches 0; Indels 45; Gaps 1;
<hr/>		
Qy	1 TTGCACTCGGCCATGTTTGGCTTCTTGCGAGCCTTGTGTGCCAGTCGAGTCGCTGGTTC	60
Dd	1 TTGCACTCGGCCATGTTTGGCTTCTTGCGAGCCTTGTGTGCCAGTCGAGTCGCTGGTTC	60
<hr/>		
Qy	61 CTTTTGGGGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCAATCTGCCCTTCAGATA	120
Dd	61 CTTTTGGGGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCAATCTGCCCTTCAGATA	120
<hr/>		
Qy	121 AAATTTCCTATGCTAGAATTACACTCCCTCAAATGTCCTCGCTGGTAGAATCTGGTCTAAA	180
Dd	121 AAATTTCCTATGCTAGAATTACACTCCCTCAAATGTCCTCGCTGGTAGAATCTGGTCTAAA	180
<hr/>		
Qy	181 GACGTCGTGTTGAAGAACTGTTCTGCGAGGTACAATTTGTCAAGGCGCCCTCGGAAATCCCC	240

	Query Match	72.8%; Score 511; DB 4; Length 1200;
	Best Local Similarity	100.0%; Pred. No. 2.2e-153;
	Matches 511; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	13 ATGTTTGGCTTCCTCGACGTGGTGTCAGACTGAGTCGTGCCTTTCCTTGGCGGG	72
Dd	1 ATGTTTGGCTTCCTCGACGTGGTGTCAGACTGAGTCGTGCCTTTCCTTGGCGGG	60
Qy	73 CTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTCCTATG	132


```
; APPLICATION NUMBER: US 60/045,233
; FILING DATE: 17-APR-1997
; APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2224
; OTHER INFORMATION: /note= "rat small conductance,
; calcium-activated potassium channel
; protein 3 (rsk3) full-length cDNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-115-415-44

Query Match 6.8%; Score 47.6; DB 4; Length 2224;
Best Local Similarity 62.7%; Pred. No. 0.0002;
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 2 TGCACCTGGCCATGTTGGCTTCTTCGACGTTGGTCCAGTCTGAGTGGTTC 61
Db 309 TGCAACAGACAGATGACAACTGGCTCTGGAGTTGGGCAAGCTGAGGCGG 250
Qy 62 TTTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 119
Db 249 AGTGGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 192

RESULT 13
US-10-116-260-44/c
; Sequence 44, Application US/10116260
; Patent No. 6828123
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses
; Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/116,260
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,590
; FILING DATE: 10-Mar-1999
; APPLICATION NUMBER: US 60/026,451

; APPLICATION NUMBER: US 60/045,233
; FILING DATE: 17-APR-1997
; APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2224
; OTHER INFORMATION: /note= "rat small conductance,
; calcium-activated potassium channel
; protein 3 (rsk3) full-length cDNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-116-260-44

Query Match 6.8%; Score 47.6; DB 4; Length 2224;
Best Local Similarity 62.7%; Pred. No. 0.0002;
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 2 TGCACCTGGCCATGTTGGCTTCTTCGACGTTGGTCCAGTCTGAGTGGTTC 61
Db 309 TGCAACAGACAGATGACAACTGGCTCTGGAGTTGGGCAAGCTGAGGCGG 250
Qy 62 TTTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 119
Db 249 AGTGGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 192

RESULT 14
US-10-115-671-44/c
; Sequence 44, Application US/10115671
; Patent No. 6828420
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses
; Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,671
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/09/254,590
; FILING DATE: 10-Mar-1999
; APPLICATION NUMBER: US 60/026,451
; FILING DATE: 11-SEP-1996
; APPLICATION NUMBER: US 60/040,052
; FILING DATE: 07-MAR-1997
; APPLICATION NUMBER: US 60/045,233
; FILING DATE: 17-APR-1997
; APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 014210-000730US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2224
; OTHER INFORMATION: /note= "rat small conductance,
; calcium-activated potassium channel
; protein 3 (rsk3) full-length cDNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-115-671-44

Query Match 6.8%; Score 47.6; DB 4; Length 2224;
Best Local Similarity 62.7%; Pred. No. 0.0002;
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 2 TGCACCTGGCCATGTTGGCTTCTTCGACGCTGGTGTCAGCTCGCTGAGTCGCTGGTTCC 61
Db |||||
309 TGCACACAGCAGGATGACAACTGCTCTGGAGTTGGGCAAGCTGAGGCGGGGTGC 250
Qy 62 TTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119
Db |||||
249 AGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192

RESULT 15
US-09-922-364A-48/c
; Sequence 48, Application US/09922364A
; Patent No. 662937
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses
; Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,364A
```

```
; FILING DATE: 03-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,590
; FILING DATE: 10-Mar-1999
; APPLICATION NUMBER: US 60/026,451
; FILING DATE: 11-SEP-1996
; APPLICATION NUMBER: US 60/040,052
; FILING DATE: 07-MAR-1997
; APPLICATION NUMBER: US 60/045,233
; FILING DATE: 17-APR-1997
; APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 014210-000730US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2462 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2462
; OTHER INFORMATION: /note= "human small conductance,
; calcium-activated potassium channel
; protein 3 (hsk3) full length cDNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-922-364A-48

Query Match 6.8%; Score 47.6; DB 4; Length 2462;
Best Local Similarity 62.7%; Pred. No. 0.00021;
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 2 TGCACTCGGCCATGTTGGCTTCTTCGACGCTGGTGTCAGCTCGCTGCTGGTTCC 61
Db |||||
571 TGACAGCAGGCAGGTCGACGGGCTGCTCTGGAGTTGGGCGAGCTGACACAGGGATGC 512
Qy 62 TTTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119
Db |||||
511 GGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 454

Search completed: September 9, 2005, 07:09:10
Job time : 353.87 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 12:35:36 ; Search time 1032.11 Seconds
(without alignments)
4026.354 Million cell updates/sec

Title: US-10-622-407-9
Perfect score: 702
Sequence: 1 ttgcaatcgccatgttgg.....ttttattgtatgaagtat 702

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	702	100.0	702	10	AAD64755 Mouse tms
2	702	100.0	702	12	ADJ45753 Murine tms
3	602	85.8	1550	10	AAD64754 Mouse tms
4	602	85.8	1550	12	ADJ45751 Murine tms
5	511	72.8	1200	10	AAD64758 Mouse tms
6	511	72.8	1200	12	ADJ45757 Murine tms
7	412	58.7	412	10	AAD64753 Mouse tms
8	412	58.7	412	12	ADJ45749 Murine tms
9	392.4	55.9	415	6	ABS69674 Novel mur
10	377.4	53.8	967	12	ADP57550 Mouse ymk
11	377.4	53.8	1509	2	AAV68046 Nucleic a
12	377.4	53.8	1509	12	ADM46622 Mouse 7P4
13	375.8	53.5	603	10	ADD33513 Mouse mit
14	253.2	36.1	357	12	ADP57563 Mouse ymk
15	221.8	31.6	1197	5	AAV73531 DNA encod
16	80.4	11.5	615	6	ABN89334 Murine TA
17	60.2	8.6	65	6	ABN55525 Mouse spl
18	48.6	6.9	403	3	ABK10240 Trinucleo
19	48.4	6.9	4248	11	ACN90396 Breast ca
20	47.6	6.8	389	3	ABK10248 Tri-nucle

C	21	47.6	6.8	1269	10	ACC68996	ACC68996 Human neu
C	22	47.6	6.8	1379	5	AAS87787	AAS87787 DNA encod
C	23	47.6	6.8	1423	10	ACC68997	ACC68997 Human neu
C	24	47.6	6.8	1776	2	AAZ23425	AAZ23425 Human Mac
C	25	47.6	6.8	2224	2	AAV35472	AAV35472 Rat rSK3
C	26	47.6	6.8	2462	2	AAV35473	AAV35473 Human hSK
C	27	47.6	6.8	3095	9	ACF03947	ACF03947 Human SK-
C	28	47.6	6.8	3095	10	ADP31740	ADP31740 Human SK-
C	29	47.2	6.7	1016	5	AAS79773	AAS79773 DNA encod
C	30	47	6.7	277	3	ABK10239	ABK10239 Trinucleo
C	31	46.8	6.7	504	4	ABL41663	ABL41663 Nucleotid
C	32	46.6	6.6	365	10	ACD94759	ACD94759 Human col
C	33	46.4	6.6	1080	4	ABL22295	ABL22295 Drosophil
C	34	46.4	6.6	5264	4	ABU22294	ABU22294 Drosophil
C	35	46.4	6.6	5824	4	ABL15249	ABL15249 Drosophil
C	36	46.4	6.6	11743	4	ABL15248	ABL15248 Drosophil
C	37	46.4	6.6	89873	13	ABD32846	ABD32846 Mouse can
C	38	46.2	6.6	1810	4	AAF84342	AAF84342 Human and
C	39	46.2	6.6	4719	12	ADJ92835	ADJ92835 Human co-
C	40	46.2	6.6	5257	6	ABV94246	ABV94246 Breast ca
C	41	46.2	6.6	5257	10	ADF56532	ADF56532 Fusion pr
C	42	46.2	6.6	5257	10	ADK67041	ADK67041 Gene #131
C	43	46.2	6.6	5830	12	ADP22722	ADP22722 Human SMA
C	44	46.2	6.6	5959	6	ABL66686	ABL66686 Lung canc
C	45	46.2	6.6	5959	6	ABK84651	ABK84651 Human CDN

ALIGNMENTS

RESULT 1
AAD64755

ID AAD64755 standard; cdna; 702 BP.

AC AAD64755;

DT 11-MAR-2004 (first entry)

DE Mouse tmst2-receptor splice variant cDNA.

XX Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
cachexia; autoimmune disease; inflammatory disease; chromosome mapping;
cancer; chromosome identification; gene therapy; antibacterial; virucide;
immunopressive; immunomodulator; antiinflammatory; antiparasitic;
cytostatic; mouse; splice variant; gene; ss.

OS Mus musculus.

PH Key Location/Qualifiers

FT CDS 13..555

FT /*tag= a

FT /product= "Mouse tmst2 receptor splice variant protein"

XX US6627199-B1.

PD 30-SEP-2003.

PF 07-JUL-2000; 2000US-00612033.

XX 09-JUL-1999; 99US-0143063P.

PA (AMGE-) AMGEN INC.

PI Saris C;

XX WPI; 2003-874309/81.

DR P-PSDB; ABW02716.

XX New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,
treating or ameliorating diseases associated with or resulting from
abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
chromosome mapping.


```

Qy 181 GACGCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCTCGGAAATCCCC 240
Db 181 GACGCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCTCGGAAATCCCC 240
Qy 241 CATACTCAAGGACAAATGTGAGAGTGTACCCAGGACATTTTCACAGAGAAAGATAATTAC 300
Db 241 CATACTCAAGGACAAATGTGAGAGTGTACCCAGGACATTTTCACAGAGAAAGATAATTAC 300
Qy 301 CTGGATGCTTGTATCTATCTTGTCCACCTGTGTATTAAGATCAGGAAATGGTGGCGACTGC 360
Db 301 CTGGATGCTTGTATCTATCTTGTCCACCTGTGTATTAAGATCAGGAAATGGTGGCGACTGC 360
Qy 361 TCAGCCACCAAGTACCGGAAATGTCAGTGGCCGAACAGGTCTTTACTACTATGACCCAAA 420
Db 361 TCAGCCACCAAGTACCGGAAATGTCAGTGGCCGAACAGGTCTTTACTACTATGACCCAAA 420
Qy 421 TTTCCAGAAATCGTCCGCCCATGTACCAAGTGTCCCAAGGATCCCTGTCTCCAGGAA 480
Db 421 TTTCCAGAAATCGTCCGCCCATGTACCAAGTGTCCCAAGGATCCCTGTCTCCAGGAA 480
Qy 481 TGCAACTCCACAGCTAAACACTGTGTGCAAGTTCATCTCTTTCAAGAAATCTGCTCAGTG 540
Db 481 TGCAACTCCACAGCTAAACACTGTGTGCAAGTTCATCTCTTTCAAGAAATCTGCTCAGTG 540
Qy 541 GCCTGGCCTATCTGAATGGTTTCACAGAGATCCCAAGAACCGGCTGTTCTTACTGTTATCA 600
Db 541 GCCTGGCCTATCTGAATGGTTTCACAGAGATCCCAAGAACCGGCTGTTCTTACTGTTATCA 600
Qy 601 CCTTTGAGTGTCTAAATGTTGTCGTTGCTCTTCCGTTATCATAGAAGATAAGGTTTC 660
Db 601 CCTTTGAGTGTCTAAATGTTGTCGTTGCTCTTCCGTTATCATAGAAGATAAGGTTTC 660
Qy 661 TACAGATGTTTCTTAGCTTCTTTTATGCTATGAAGTGAT 702
Db 661 TACAGATGTTTCTTAGCTTCTTTTATGCTATGAAGTGAT 702

RESULT 3
AD64754
ID AAD64754 standard; cDNA; 1550 BP.
XX
AC AAD64754;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mouse tmst2-receptor cDNA.
XX
KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;
KW cancer; chromosome identification; gene therapy; antibacterial; virucide;
KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
KW cyostatic; mouse; gene; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 13..609
FT /*tag= a
FT /product= "Mouse tmst2 receptor protein"
XX
US6627199-B1.
XX
PN 30-SEP-2003.
XX
XX 07-JUL-2000; 2000US-00612033.
XX
XX 09-JUL-1999; 99US-0143063P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Saris C;
XX

```

DR WPI; 2003-874309/81.
 DR P-PSDB; ABW02715.

PT New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,
 PT treating or ameliorating diseases associated with or resulting from
 PT abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
 PT chromosome mapping.

XX Claim 1; SEQ ID NO 7; Opp; English.

PS The invention relates to transmembrane decoy-receptor (tmst2) proteins
 CC and their secreted splice variants, belonging to the tumour necrosis
 CC factor (TNF) receptor super gene family and polynucleotides encoding such
 CC or proteins. The composition and methods are useful in diagnosing, treating
 CC or ameliorating diseases associated with or resulting from abnormal tmst2
 CC and/or abnormal expression of its putative ligand, such as sepsis,
 CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial
 CC and parasitic diseases or cancer. They may also be used for chromosome
 CC identification or mapping. The invention is useful in gene therapy. The
 CC present sequence is mouse tmst2-receptor cDNA used in the exemplification
 CC of the invention

XX SQ Sequence 1550 BP; 400 A; 401 C; 299 G; 450 T; 0 U; 0 Other;

Query Match 85.8%; Score 602; DB 10; Length 1550;

Best Local Similarity 93.6%; Pred. No. 4.9e-163;

Matches 657; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

Qy 1 TTGCACCTCGGCCCATGTTTGGCTTCTTCTGCAGCTGCTGTCAGTCTGAGTCCGCTGCTTC 60

Db 1 TTGCACCTCGGCCCATGTTTGGCTTCTTCTGCAGCTGCTGTCAGTCTGAGTCCGCTGCTTC 60

Qy 61 CTTTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

Db 61 CTTTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

Qy 121 AAATTTGCTATGCTAGAAATACACTCTCTTCAAAATGTCCTGCTGCTGCTGCTGCTGCTGCT 180

Db 121 AAATTTGCTATGCTAGAAATACACTCTCTTCAAAATGTCCTGCTGCTGCTGCTGCTGCTGCT 180

Qy 181 GACGCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCTCGGAAATCCCC 240

Db 181 GACGCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCTCGGAAATCCCC 240

Qy 241 CATACTCAAGGACAAATGTGAGAGTGTACCCAGGACATTTTCACAGAGAAAGATAATTAC 300

Db 241 CATACTCAAGGACAAATGTGAGAGTGTACCCAGGACATTTTCACAGAGAAAGATAATTAC 300

Qy 301 CTGGATGCTTGTATCTATCTTGTCCACCTGTGTATTAAGATCAGGAAATGGTGGCGACTGC 360

Db 301 CTGGATGCTTGTATCTATCTTGTCCACCTGTGTATTAAGATCAGGAAATGGTGGCGACTGC 360

Qy 361 TCAGCCACCAAGTACCGGAAATGTCAGTGGCCGAACAGGTCTTTACTACTATGACCCAAA 420

Db 361 TCAGCCACCAAGTACCGGAAATGTCAGTGGCCGAACAGGTCTTTACTACTATGACCCAAA 420

Qy 421 TTTCCAGAAATCGTCCGCCCATGTACCAAGTGTCCCAAGGATCCCTGTCTCCAGGAA 480

Db 421 TTTCCAGAAATCGTCCGCCCATGTACCAAGTGTCCCAAGGATCCCTGTCTCCAGGAA 480

Qy 481 TGCAACTCCACAGCTAAACACTGTGTGCAAGTTCATCTCTTTCAAGAAATCTGCTCAGTG 540

Db 481 TGCAACTCCACAGCTAAACACTGTGTGCAAGTTCATCTCTTTCAAGAAATCTGCTCAGTG 540

Qy 541 GCCTGGCCTATCTGAATGGTTTCACAGAGATCCCAAGAACCGGCTGTTCTTACTGTTATCA 600

Db 541 GCCTGGCCTATCTGAATGGTTTCACAGAGATCCCAAGAACCGGCTGTTCTTACTGTTATCA 600

Qy 601 CCTTTGAGTGTCTAAATGTTGTCGTTGCTCTTCCGTTATCATAGAAGATAAGGTTTC 660

Db 601 CCTTTGAGTGTCTAAATGTTGTCGTTGCTCTTCCGTTATCATAGAAGATAAGGTTTC 660

Qy 661 TACAGATGTTTCTTAGCTTCTTTTATGCTATGAAGTGAT 702

Db 661 TACAGATGTTTCTTAGCTTCTTTTATGCTATGAAGTGAT 702

```

Db      616 TACAGATGTTTCTTAGCTTCTCTTTATGCTAAGATGAT 657
|||||
RESULT 4
ADJ45751
ID      ADJ45751 standard; cDNA; 1550 BP.
XX
AC      ADJ45751;
XX
DT      06-MAY-2004 (first entry)
XX
DE      Murine tmst2-receptor cDNA.
XX
KW      Mouse; tmst2-receptor; gene; ss; acquired immunodeficiency syndrome;
KW      AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria;
KW      diabetes mellitus; disseminated intravascular coagulation;
KW      haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;
KW      lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;
KW      organ rejection; rheumatoid arthritis; septic shock; stroke;
KW      adult respiratory distress syndrome; ARDS; tuberculosis; viral disease.
XX
OS      Mus musculus.
XX
FH      Key Location/Qualifiers
FT      CDS 13..609
FT      /*tag= a
FT      /product= "Murine tmst2-receptor"
XX
XX      US2004018544-A1.
XX      29-JAN-2004.
XX
XX      17-JUL-2003; 2003US-00622407.
XX
XX      09-JUL-1999; 99US-0143063P.
XX      07-JUL-2000; 2000US-00612033.
XX
XX      (SARI/) SARIS C.
XX
XX      Saxis C;
XX
XX      WPI; 2004-224390/21.
XX      P-PSDB; ADJ45752.
XX
XX      Novel tmst2-receptor polypeptide useful for diagnosing and treating
XX      disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
XX      infections.
XX
XX      Claim 1; SEQ ID NO 7; 57pp; English.
XX
XX      The invention relates to a tmst2-receptor polypeptides and the
XX      polynucleotide encoding them. The sequences of the invention are useful
XX      for treating diseases and conditions including acquired immunodeficiency
XX      syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral
XX      malaria, diabetes mellitus, disseminated intravascular coagulation,
XX      haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,
XX      lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ
XX      rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory
XX      distress syndrome (ARDS), tuberculosis and a number of viral diseases.
XX      This sequence represents cDNA encoding the murine tmst2-receptor
XX      polypeptide of the invention.
XX
XX      Query Match 85.8%; Score 602; DB 12; Length 1550;
XX      Best Local Similarity 93.6%; Pred. No. 4.9e-163;
XX      Matches 657; Conservative 0; Mismatches 0; Indels 45; Gaps 1;
XX
Qy      1 TTGCACCTCGGCGATGTTGGTTCTTCTGACAGTTGGTGCCAGTCGTGAGTCGCTGTTTC 60
Db      1 TTGCACCTCGGCGATGTTGGTTCTTCTGACAGTTGGTGTCAGTCGTGAGTCGCTGTTTC 60

```


301 C TGGAGTCCTGGTATACCTTGGCTCCACCTGGTAAAGATCAGGAAAATGGTGGCCGACATGC 36

XX

DK F-FSDB; ADF3/331.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

XX	Key	Location/Qualifiers
FH		

[illegible]

RESULT 15
AAS73531

Db 417 CCCCCATCTCAAGGACAATGTGAGAGTGTACCCAGGAACATTCACAGAGAAAGATAA 476
Qy 297 TTACCTGGATGCTTGTATATACTTTGCTCCACCTGTGTATAAAGATCA 341
Db 477 TTACCTGGATGCTTGTATATACTTTGCTCCACCTGTGTATAAAGGTGA 521

Search completed: September 8, 2005, 17:05:23
Job time : 1034.11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 16:10:01 ; Search time 1594.46 Seconds
(without alignments)
2891.383 Million cell updates/sec

Title: US-10-622-407-9

Perfect score: 702

Sequence: 1 ttgcatcgccatgttggtttg.....ttttattgtatgaatgat 702

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*

18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*

19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*

20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*

21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*

22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq.*

23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*

24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*

25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	702	100.0	702	US-10-622-407-9
2	602	85.8	17	US-10-622-407-7
3	511	72.8	1200	US-10-622-407-13
4	412	58.7	412	US-10-622-407-5
5	392.4	55.9	415	US-09-728-445-737
6	392.4	55.9	415	US-10-964-549-737
7	377.4	53.8	967	US-10-193-616-7
				Sequence 9, Appli
				Sequence 7, Appli
				Sequence 13, Appli
				Sequence 5, Appli
				Sequence 737, App
				Sequence 737, App
				Sequence 7, Appli

8	377.4	53.8	1509	9	US-09-855-266A-3	Sequence 3, Appli
9	377.4	53.8	1509	19	US-10-802-332-3	Sequence 3, Appli
10	253.2	36.1	357	14	US-10-193-616-5	Sequence 5, Appli
11	60.2	8.6	65	10	US-09-908-975-28273	Sequence 28273, A
12	48.4	6.9	4248	14	US-10-198-846-11546	Sequence 11546, A
13	47.6	6.8	1269	20	US-10-489-372-43	Sequence 43, Appli
14	47.6	6.8	1423	20	US-10-489-372-44	Sequence 44, Appli
15	47.6	6.8	2224	9	US-09-922-364A-44	Sequence 44, Appli
16	47.6	6.8	2224	9	US-09-254-590-44	Sequence 44, Appli
17	47.6	6.8	2224	13	US-10-115-695-44	Sequence 44, Appli
18	47.6	6.8	2224	14	US-10-116-561-44	Sequence 44, Appli
19	47.6	6.8	2224	14	US-10-115-671-44	Sequence 44, Appli
20	47.6	6.8	2224	14	US-10-115-415-44	Sequence 44, Appli
21	47.6	6.8	2224	14	US-10-116-260-44	Sequence 44, Appli
22	47.6	6.8	2224	15	US-10-115-688-44	Sequence 44, Appli
23	47.6	6.8	2393	21	US-10-278-698-70	Sequence 70, Appli
24	47.6	6.8	2393	21	US-10-278-698-584	Sequence 584, App
25	47.6	6.8	2462	9	US-09-922-364A-48	Sequence 48, Appli
26	47.6	6.8	2462	9	US-09-254-590-48	Sequence 48, Appli
27	47.6	6.8	2462	13	US-10-115-695-48	Sequence 48, Appli
28	47.6	6.8	2462	14	US-10-116-561-48	Sequence 48, Appli
29	47.6	6.8	2462	14	US-10-115-671-48	Sequence 48, Appli
30	47.6	6.8	2462	14	US-10-115-415-48	Sequence 48, Appli
31	47.6	6.8	2462	14	US-10-116-260-48	Sequence 48, Appli
32	47.6	6.8	2462	15	US-10-115-688-48	Sequence 48, Appli
33	46.4	6.6	89873	21	US-10-353-690-97	Sequence 97, Appli
34	46.4	6.6	89873	21	US-10-461-862-61	Sequence 61, Appli
35	46.2	6.6	4719	17	US-10-414-692-36	Sequence 36, Appli
36	46.2	6.6	5257	15	US-10-007-926A-237	Sequence 237, App
37	46.2	6.6	5257	21	US-10-956-157-995	Sequence 995, App
38	46.2	6.6	5864	21	US-10-956-157-4070	Sequence 1996, Ap
39	46.2	6.6	5959	9	US-09-954-456-1996	Sequence 5023, Ap
40	46.2	6.6	5959	21	US-10-843-641A-5023	Sequence 26238, A
41	46	6.6	2045	18	US-10-425-114-26238	Sequence 103, App
42	46	6.6	2770	20	US-10-737-450-103	Sequence 475, App
43	46	6.6	3302	15	US-10-037-270-475	Sequence 475, App
44	46	6.6	3302	17	US-10-117-722-475	Sequence 26, Appli
45	46	6.6	3895	19	US-10-618-941-26	

ALIGNMENTS

RESULT 1

US-10-622-407-9

; Sequence 9, Application US/10622407

; Publication No. US20040018544A1

; GENERAL INFORMATION:

; APPLICANT: Saris, Chris

; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TM2T2, A NOVEL

; FILE REFERENCE: 01017/35434B

; CURRENT APPLICATION NUMBER: US/10/622,407

; CURRENT FILING DATE: 2003-07-17

; PRIOR APPLICATION NUMBER: US 09/612,033

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,063

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9

; LENGTH: 702

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (13)..(552)

; FEATURE:

; OTHER INFORMATION: Primer 2086-39

US-10-622-407-9

Query Match 100.0%; Score 702; DB 17; Length 702;
Best Local Similarity 100.0%; Pred. No. 7.1e-211;

PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 1200
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion protein consisting of Mus musculus sequences and Immunoglobulin sequences
NAME/KEY: CDS
LOCATION: (1)..(1194)
US-10-622-407-13

Query Match 72.8%; Score 511; DB 17; Length 1200;
Best Local Similarity 100.0%; Pred. No. 2.3e-150; Indels 0; Gaps 0;
Matches 511; Conservative 0; Mismatches 0;

QY 13 ATGTTTGGCTTCCTCAGCTTGCGTGCAGTCTGAGTCGCTGGTTCCTTTGCGCGCGG 72
DB 1 ATGTTTGGCTTCCTCAGCTTGCGTGCAGTCTGAGTCGCTGGTTCCTTTGCGCGCGG 60
QY 73 CTGCTGTGCTGTGCTGTGCTGTGCTGTGAATCTGCCCTTGCAAGTAATAATTGCTATG 132
DB 61 CTGCTGTGCTGTGCTGTGCTGTGCTGTGAATCTGCCCTTGCAAGTAATAATTGCTATG 120
QY 133 CTAGAATTACACTCCCTCAAAATCTCCCGCTGGTGAATCTGCTCTAAGACGCTCTGTGC 192
DB 121 CTAGAATTACACTCCCTCAAAATCTCCCGCTGGTGAATCTGCTCTAAGACGCTCTGTGC 180
QY 193 AAGAACTGTTCTGCAGGTACAATTTGTCAAGCGCGCCCTGCCAAAATCCCCCATCTCAAGGA 252
DB 181 AAGAACTGTTCTGCAGGTACAATTTGTCAAGCGCGCCCTGCCAAAATCCCCCATCTCAAGGA 240
QY 253 CAATGTGAGAAGTGTACCACGAGAACATTCACAGAGAAAGATAATTAACCTGGATGCTTGT 312
DB 241 CAATGTGAGAAGTGTACCACGAGAACATTCACAGAGAAAGATAATTAACCTGGATGCTTGT 300
QY 313 ATACTTTGCTCCACCTGTGTGAATGATCAGGAATGGTGGCCGACTGCTCAGCCACCACT 372
DB 301 ATACTTTGCTCCACCTGTGTGAATGATCAGGAATGGTGGCCGACTGCTCAGCCACCACT 360
QY 373 GACCGGAAATGCCAGTGCAGTCCGAAACAGGTCTTTACTATGACCCCAAATTTCCAGAAATCG 432
DB 361 GACCGGAAATGCCAGTGCAGTCCGAAACAGGTCTTTACTATGACCCCAAATTTCCAGAAATCG 420
QY 433 TGGCGGCCATGTATACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACA 492
DB 421 TGGCGGCCATGTATACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACA 480
QY 493 GCTAACTCTGTGTCAGTTTCATCTGTTTTCAA 523
DB 481 GCTAACTCTGTGTCAGTTTCATCTGTTTTCAA 511

RESULT 4
US-10-622-407-5
Sequence 5, Application US/10622407
Publication No. US20040018544A1
GENERAL INFORMATION:
APPLICANT: Sarsis, Chris
TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
FILE REFERENCE: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US 09/612,033
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15

[illegible]

[illegible]

; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
 ; FILE REFERENCE: 01017/35551A
 ; CURRENT APPLICATION NUMBER: US/10/193,616
 ; CURRENT FILING DATE: 2002-07-11
 ; PRIOR APPLICATION NUMBER: US/09/611,989
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 60/143,137
 ; PRIOR FILING DATE: 1999-07-07
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 357
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (6)..(356)
 US-10-193-616-5

	Query Match	Best Local Similarity	Score	DB 14;	Length	357;	Mismatches	Indels	Gaps	0;
Qy	81	GCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTCAGAGTAAATTGCTATGCTAGAATT	140							
Dd	44	GTTCCTCTTGCTGCTGCTGCTGAATCTGTTCTTGCCTCGTAATATTTGCTATGCTGAATC	103							
Qy	141	ACACTCTCTCAAAATGTCCTGGCTGGTGAATACCTGGTCTAAAAGACGTCCTGTCGAAGAACTG	200							
Dd	104	ATACTCTCTCAACTGTCCTGGATGTAATACAGTCTAATGATGTCCTGTCGAAGACCTG	163							
Qy	201	TTCCTGAGGTACATTTGTCAGGGCCCTCGGAAATCCCCCATCTCAAGGACAATGTGA	260							
Dd	164	TCCCTCAGGTACATTTGTCAGGGCCCTCGCAAATCCCCCATCTCAAGGACAATGTGA	223							
Qy	261	GAATGTTCACCCAGGACCAATTCACAGAGAAAGATAATTAATCTGTAATCTTTG	320							
Dd	224	GAATGTTCACCCAGGACCAATTCACAGGAGAAAGATAATGGCTGTCATGATTTGTAATCTTTG	283							
Qy	321	CTCCACCTGTGATAAAGATCAGGAATGCTGGCCGACCTGCTCAGGCCACCAGTGACCGAA	380							
Dd	284	CTCCACCTGTGATAAAGACCAAGATAATGGTGGCTGACTGTTCTGCCACCAGTGACCGAA	343							
Qy	381	ATGCCAGTGCCGAA	394							
Dd	344	ATGCCAGTGCCAAA	357							

RESULT 11
 US-09-908-975-28273
 ; Sequence 28273, Application US/09908975
 ; Publication No. US20030165843A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SHOSHAN, Avi
 ; APPLICANT: WASSERMAN, Alon
 ; APPLICANT: MINTZ, Eli
 ; APPLICANT: MINTZ, Liat
 ; APPLICANT: FAIGLER, Simchon
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
 ; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
 ; FILE REFERENCE: 36688-0005
 ; CURRENT APPLICATION NUMBER: US/09/908,975
 ; CURRENT FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: US 60/287,724
 ; PRIOR FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: US 60/221,607
 ; PRIOR FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 32337
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 28273
 ; LENGTH: 65
 ; TYPE: DNA
 ; ORGANISM: Mus musculus

```

; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: TRAN, Uyen K.
; APPLICANT: LEHR-MASON, Patricia M.
; APPLICANT: TANG, Y. Tom
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: KABLE, Amy E.
; APPLICANT: CHANG, Hsin-Ru
; APPLICANT: KHARE, Reena
; APPLICANT: BECHA, Shanya D.
; APPLICANT: JIN, Pei
; APPLICANT: LEE, Sally
; TITLE OF INVENTION: NEUROTRANSMISSION-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1185 USN
; CURRENT APPLICATION NUMBER: US/10/489,372
; CURRENT FILING DATE: 2004-03-12
; PRIOR FILING DATE: 2001-09-14
; PRIOR FILING DATE: 2001-09-28
; PRIOR FILING DATE: 2001-10-04
; PRIOR FILING DATE: 2001-11-27
; PRIOR FILING DATE: 2001-12-07
; PRIOR FILING DATE: 2002-01-04
; PRIOR FILING DATE: 2002-03-18
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PERL Program
; SEQ ID NO 43
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7505818CB1
US-10-489-372-43

Query Match      6.8%; Score 47.6; DB 20; Length 1269;
Best Local Similarity 66.7%; Pred. No. 0.00075;
Matches 68; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 18 TGGCTTCTTCGACGCTTGGTCCAGTCGTCGAGTCGTCGTCCTTTGGCGGGCGCTGCT 77
Db 901 TGGCTGGCCCTTCACATGGAATGAACTCTGCTGATAGTCCCTGCTGCTGCTGCT 842

Qy 78 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119
Db 841 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800

RESULT 14
US-10-489-372-44/c
; Sequence 44, Application US/10489372
; Publication No. US20040203014A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HONCHELL, Cynthia D.
; APPLICANT: WARREN, Bridget A.

```

```

; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: LI, Joana X.
; APPLICANT: LEE, Soo Yeun
; APPLICANT: YUE, Henry
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: MARQUIS, Joseph P.
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: TRAN, Uyen K.
; APPLICANT: LEHR-MASON, Patricia M.
; APPLICANT: TANG, Y. Tom
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: KABLE, Amy E.
; APPLICANT: CHANG, Hsin-Ru
; APPLICANT: KHARE, Reena
; APPLICANT: BECHA, Shanya D.
; APPLICANT: JIN, Pei
; APPLICANT: LEE, Sally
; TITLE OF INVENTION: NEUROTRANSMISSION-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1185 USN
; CURRENT APPLICATION NUMBER: US/10/489,372
; CURRENT FILING DATE: 2004-03-12
; PRIOR FILING DATE: 2001-09-14
; PRIOR FILING DATE: 2001-09-28
; PRIOR FILING DATE: 2001-10-04
; PRIOR FILING DATE: 2001-10-26
; PRIOR FILING DATE: 2001-11-02
; PRIOR FILING DATE: 2001-11-27
; PRIOR FILING DATE: 2001-12-07
; PRIOR FILING DATE: 2002-01-04
; PRIOR FILING DATE: 2002-03-18
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PERL Program
; SEQ ID NO 44
; LENGTH: 1423
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7505821CB1
US-10-489-372-44

Query Match      6.8%; Score 47.6; DB 20; Length 1423;
Best Local Similarity 66.7%; Pred. No. 0.0008;
Matches 68; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 18 TGGCTTCTTCGACGCTTGGTCCAGTCGTCGAGTCGTCGTCCTTTGGCGGGCGCTGCT 77
Db 985 TGGCTGGCCCTTCACATGGAATGAACTCTGCTGATAGTCCCTGCTGCTGCTGCT 925

Qy 78 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119
Db 925 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 884

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 13:43:46 ; Search time 8202.37 Seconds
(without alignments)
3257.733 Million cell updates/sec

Title: US-10-622-407-9
Perfect score: 702
Sequence: 1 ttgcactcgccatgttgg.....ttttattgtatgaagtgat 702

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	697	99.3	2276	3 AK012838	AK012838 Mus muscu
2	694	98.9	1003	6 BY711952	BY711952 BY711952
3	602	85.8	765	7 CN461442	CN461442 UI-M-HB0-
4	602	85.8	4224	3 BC076592	BC076592 Mus muscu
5	573.4	81.7	696	5 BU611594	BU611594 UI-M-F10-
6	571	80.1	708	6 CB525851	CB525851 UI-M-FY0-
7	562	80.1	784	6 CB723050	CB723050 UI-M-GH0-
8	539	76.8	683	7 CF729486	CF729486 UI-M-HD0-
9	403	57.4	410	9 CG651536	CG651536 OST12784
10	392.4	55.9	415	9 CS535649	CS535649 OST122794
11	375.8	53.5	639	4 BG077775	BG077775 H3019T06-
12	358.8	51.1	585	2 BB613091	BB613091 BB613091
13	354.6	50.5	614	7 CN687949	CN687949 E0250A07-
14	353.6	50.4	597	7 CN697902	CN697902 E0401A05-
15	316.4	45.1	371	5 BY182663	BY182663 BY182663
16	315.8	45.0	489	7 CK333918	CK333918 H8266D02-
17	304.2	43.3	331	5 BY343934	BY343934 BY343934
18	301	42.9	351	5 BY208766	BY208766 BY208766
19	295	42.0	317	5 BY345556	BY345556 BY345556
20	278.4	39.7	410	5 BY183172	BY183172 BY183172
21	266.4	37.9	331	5 BY195969	BY195969 BY195969
22	263.4	33.2	346	5 BY010018	BY010018 BY010018
23	232.8	33.2	347	2 BB873121	BB873121 BB873121
24	229.4	32.7	341	5 BY036522	BY036522 BY036522

25	223	31.8	338	5	BY325940	BY325940
26	210	29.9	544	1	AI747041	AI747041 u112901.Y
27	208.2	29.7	320	5	BY181385	BY181385 BY181385
28	208.2	29.7	333	5	BY175331	BY175331 BY175331
29	208.2	29.7	340	5	BY187354	BY187354 BY187354
30	208.2	29.7	355	5	BY177525	BY177525 BY177525
31	193	27.5	296	5	BY142271	BY142271 BY142271
32	190.2	27.1	235	7	CN688320	CN688320 E0256E11-
33	189.2	27.0	210	7	CK342400	CK342400 K0430A11-
34	181.4	25.8	403	5	BY201915	BY201915 BY201915
35	152.8	21.8	664	6	CD469537	CD469537 Leuko82.4
36	119.4	17.0	607	8	AQ927517	AQ927517 RPCI-23-2
37	110.4	15.7	599	8	AZ405040	AZ405040 IM0173F02
38	102	14.5	756	7	CK634366	CK634366 UI-M-HN0-
39	94.8	13.5	763	9	AG478921	AG478921 Mus muscu
40	91	13.0	709	9	BX969828	BX969828 Forward s
41	87	12.4	742	6	C82050	C82050 C82050 Leuk
42	87	12.4	900	6	C82250	C82250 C82250 Leuk
43	86	12.3	741	1	AU050103	AU050103 AU050103
44	85.4	12.2	747	1	AU050106	AU050106 AU050106
45	80.4	11.5	719	6	BY748342	BY748342 BY748342

ALIGNMENTS

RESULT 1
LOCUS AK012838 2276 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810028K06 product:Tumor necrosis factor receptor superfamily member 21, full insert sequence.
ACCESSION AK012838
VERSION AK012838.1 GI:12849843
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636
REFERENCE 2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED 11042159
REFERENCE 3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED 11076861
REFERENCE 4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
The FANTOM Consortium and the RIKEN Genome Exploration Research


```

FEATURES
  source
    Seq primer: pYX-5
    Location/Qualifiers
      1..765
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="C57BL/6"
        /db_xref="taxon:10090"
        /clone="IMAGE:30652769"
        /tissue_type="whole eye"
        /dev_stages="embryo 12.5,13.5,14.5 dpc"
        /lab_host="DH10B (T1 phage resistant)"
        /clone_lib="NTH BMAP HBO"
        /note="Organ: Eye, Vector: pYX-Asc; Site 1: EcoR I;
        Site 2: Not I; The library was constructed according
        Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
        1996. Denatured RNA was size fractionated on a 1% agarose
        gel. First strand cDNA synthesis was primed with oligo-dT
        primer containing a Not I site. Double strand cDNA was
        size selected according to mRNA size fraction, ligated
        with EcoR I adaptor, digested with NotI and then cloned
        directionally into pYX-Asc vector. The library tag
        sequence located between the Not I site and the polyA tail
        is TATGTGAAGT. This library was created for the University
        Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
        Developing Mouse Nervous System', supported by National
        Institute of Mental Health (NIMH)."
```

Query Match 85.8%; Score 602; DB 7; Length 765;
Best Local Similarity 93.6%; Pred. No. 1.9e-163;
Matches 657; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

Qy 1 TTGCACCTGGCCATGTTGGCTTCTTCGACGTTGGTGTCCAGCTGAGTCGCTGTTTC 60
Db 10 TTGCACCTGGCCATGTTGGCTTCTTCGACGTTGGTGTCCAGCTGAGTCGCTGTTTC 69
Qy 61 CTTTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 70 CTTTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129
Qy 121 AAATTTGCTATGTAGAAATTACATCTCTTCAAAATGTCCTGCTGCTGCTGCTGCTGCT 180
Db 130 AAATTTGCTATGTAGAAATTACATCTCTTCAAAATGTCCTGCTGCTGCTGCTGCTGCT 189
Qy 181 GACGCTGTTGCAAGAACTGTTTTCGACGTTACATTTGTCAGGCGCCCTGCGAAATCCCC 240
Db 190 GACGCTGTTGCAAGAACTGTTTTCGACGTTACATTTGTCAGGCGCCCTGCGAAATCCCC 249
Qy 241 CATACTCAAGACAAATGTGAGAGTGTACCCAGGACATTTACAGAGAAAGATAATTAC 300
Db 250 CATACTCAAGACAAATGTGAGAGTGTACCCAGGACATTTACAGAGAAAGATAATTAC 309
Qy 301 CTGGATGCTTGTATCTTTGCTCCACCTGTGTATAAAGATCAGGAAATGGTGGCCGACTGC 360
Db 310 CTGGATGCTTGTATCTTTGCTCCACCTGTGTATAAAGATCAGGAAATGGTGGCCGACTGC 369
Qy 361 TCAGCCACCAAGTACCGGAAATGCGAGTGGCGGAAACAGGTCTTTACTACTATGACCCAAA 420
Db 370 TCAGCCACCAAGTACCGGAAATGCGAGTGGCGGAAACAGGTCTTTACTACTATGACCCAAA 429
Qy 421 TTTTCAGAAATGTCGCGCCCATGTACCAAGTGTCCCAAGAAATCCCTGTCTCTCCAGAA 480
Db 430 TTTTCAGAAATGTCGCGCCCATGTACCAAGTGTCCCAAGAAATCCCTGTCTCTCCAGAA 489
Qy 481 TGCAACTCCACAGCTAAACACTGTGTGCAAGTTCATCTGTTTCAAGAAATCTGCTCAGTG 540
Db 490 TGCAACTCCACAGCTAAACACTGTGTGCAAGTTCATCTGTTTCAAGAAATCTGCTCAGTG 532
Qy 541 GCCTGGCCTATCTGAAATGGTTTCAAGAGATCCCAAGAAACCGGCTGTTTCTACTGTTATCA 600
Db 533 -----ATCCAGAAACCGGCTGTTTCTACTGTTATCA 564
Qy 601 CCTTTGAGTGTCTAATTGTGTCGTTGTTGCTTCCGTATCATAGAGATAAGGTTTC 660

Db 565 CCTTTGAGTGTCTAATTGTGTCGTTGTTGCTTCCGTATCATAGAGATAAGGTTTC 624
Qy 661 TACAGATGTTTCTTACGTTCCCTTTTATTTGCTATGAAGTGTAT 702
Db 625 TACAGATGTTTCTTACGTTCCCTTTTATTTGCTATGAAGTGTAT 666

RESULT 4
BC076592 4224 bp mRNA linear HTC 27-JUL-2004
LOCUS BC076592
DEFINITION Mus musculus tumor necrosis factor receptor superfamily, member 22,
mRNA (cDNA clone IMAGE:30652769).
VERSION BC076592.1 GI:50370338
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4224)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettaman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,R., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 4224)
Strausberg,R.
Direct Submission
Submitted (06-JUL-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-x@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: <http://genome.uiowa.edu>
Contact: bento-soares@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: Place: Row: Column: 0
This clone has the following problem: clone inconsistent with known
gene structure.
Location/Qualifiers
1..4224
/organism="Mus musculus"

FEATURES
source


```

|||||
301 TGTGATAAGATCAGGAATGTCGCCACTGCTCAGCCACAGTGACCGGAAATGCCAG 360
|||||
388 TGCCGAACAGGCTTTTACTACTATGACCCAAATTTCCAGAAATGTCGCCGCAATGACC 447
|||||
361 TGCCGAACAGGCTTTTACTACTATGACTCAAAATTTCCAGAAATGTCGCCGCAATGACC 420
|||||
448 AAGTGTCCTCCCAAGGAATCCCTGCTCTCCAGAAATGCAACTCCACAGCTTAACACTGTGTC 507
|||||
421 AAGTGTCCTCCCAAGGAATCCCTGCTCTCCAGAAATGCAACTCCACAGCTTAACACTGTGTC 480
|||||
508 AGTTTCATCTGTTTCAAGAAATCTGCCTCAGTCGGCCTCTATCTGAATGGTTTCACAGA 567
|||||
481 AGTTTCATCTGTTTCAA----- 496
|||||
568 GATCCCAAGAACCCGCTGCTCTACTGTTATCACCCTTTGAGTGCTAAATGTCGCTT 627
|||||
497 -ATCCAGAACCCGCTGCTCTACTGTTATCACCCTTTGAGTGCTAAATGTCGCTT 555
|||||
628 GTTGCTTCCGTATCATGAAGATAAAGGTTCTACAGATGTTTCTTACGCTTCTTTT 687
|||||
556 GTTGCTTCCGTATCATGAAGATAAAGGTTCTACAGATGTTTCTTACGCTTCTTTT 615
|||||
688 TTGCTATGAAGTGAT 702
|||||
616 TTGCTATGAAGTGAT 630

```

RESULT 6

CB525851
LOCUS
DEFINITION
UI-M-FY0-cfe-p-15-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE:6848608 5', mRNA sequence.

CB525851

EST.
CB525851.1 GI:29359322

KEYWORDS
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 708)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

cDNA Library preparation: Dr. Jim Lin, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

The following repetitive elements were found in this cDNA

sequence: 35-71, >(CAG)n#simple_repeat (matched complement)

643-670, >(TAAA)n#simple_repeat (matched complement)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1..708

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6848608"

/tissue_type="whole brain"

/dev_stage="embryo 13.5, 14.5, 15.5, 16.5, 17.5dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP_FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;

Site 2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 81.3%; Score 571; DB 6; Length 708;
Best Local Similarity 93.3%; Pred. No. 1.9e-154;
Matches 626; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

Qy 32 GCTTGGTGTCCAGTCTGAGTGGCTGCTCTTTGGCGCGGCTGCTGCTGCTGCTGTC 91
Db |||||||
Qy 1 GCTTGGTGTCCAGTCTGAGTGGCTGCTCTTTGGCGCGGCTGCTGCTGCTGTC 60
Db |||||||
Qy 92 TGTCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGCTATGCTAGAAATTACACTCCTTCA 151
Db |||||||
Qy 61 TGTCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGCTATGCTAGAAATTACACTCCTTCA 120
Db |||||||
Qy 152 AATGTCCTGCTGCTGAATCTGCTGCTAAAGACGCTGCTGCTGCAAGAACTGTTCTCGAGTA 211
Db |||||||
Qy 121 AATGTCCTGCTGCTGAATCTGCTGCTAAAGACGCTGCTGCTGCAAGAACTGTTCTCGAGTA 180
Db |||||||
Qy 212 CATTTGTCAAGGCGCCCTCGGAATCCCATCTCAAGACATGTGAGAACTGTCAC 271
Db |||||||
Qy 181 CATTTGTCAAGGCGCCCTCGGAATCCCATCTCAAGACATGTGAGAACTGTCAC 240
Db |||||||
Qy 272 CAGGAACATTCACAGAGAAAGATAATTAACCTGGAATGCTGTATATCTTTGCTCCACCTGTG 331
Db |||||||
Qy 241 CAGGAACATTCACAGAGAAAGATAATTAACCTGGAATGCTGTATATCTTTGCTCCACCTGTG 300
Db |||||||
Qy 332 ATAAAGATCAGGAATAATGGTGGCCGACTGCTGAGCCACAGTACCCGAAATGCCAGTGCC 391
Db |||||||
Qy 301 ATAAAGATCAGGAATAATGGTGGCCGACTGCTGAGCCACAGTACCCGAAATGCCAGTGCC 360
Db |||||||
Qy 392 GACAGGCTCTTACTACTATGACCCCAAAATTTCCAGAACTGTCGCCGCTATGTACCAAGT 451
Db |||||||
Qy 361 GACAGGCTCTTACTACTATGACCCCAAAATTTCCAGAACTGTCGCCGCTATGTACCAAGT 420
Db |||||||
Qy 452 GTCCCCAAGGAATCCCTGCTCTCCAGGAATGCAACTCCACAGCTTAACACTGTGTGCAAGT 511
Db |||||||
Qy 421 GTCCCCAAGGAATCCCTGCTCTCCAGGAATGCAACTCCACAGCTTAACACTGTGTGCAAGT 480
Db |||||||
Qy 512 CATCTGTTTCAAGAAATATGCTGCTCAGTGGCCTATCTGATGGTTTCACAGATC 571
Db |||||||
Qy 481 CATCTGTTTCAA-----ATC 495
Db |||||||
Qy 572 CCAGAAACCGGCTGCTCTACTGTTATCAGCTTTGAGTGTGCTAATTTGTCGCTGTTG 631
Db |||||||
Qy 496 CCAGAAACCGGCTGCTCTACTGTTATCAGCTTTGAGTGTGCTAATTTGTCGCTGTTG 555
Db |||||||
Qy 632 TCTTCCGTTATCATAAGAAATAAAGGTTCTACAGATGTTTCTTACGATCTCTTTTATGTC 691
Db |||||||
Qy 556 TCTTCCGTTATCATAAGAAATAAAGGTTCTACAGATGTTTCTTACGATCTCTTTTATGTC 615
Db |||||||
Qy 692 TATGAAGTGAT 702
Db |||||||
Qy 616 TATGAAGTGAT 626

RESULT 7

CB723050

LOCUS

DEFINITION

UI-M-GH0-cel-e-02-0-UI.r1 NIH BMAP_GH0 Mus musculus cDNA clone

IMAGE:6841035 5', mRNA sequence.

CB723050

ACCESSION

VERSION

CB723050 784 bp mRNA linear EST 09-JUL-2003
UI-M-GH0-cel-e-02-0-UI.r1 NIH BMAP_GH0 Mus musculus cDNA clone
IMAGE:6841035 5', mRNA sequence.
CB723050
CB723050.1 GI:29780192

[illegible]

Db 418 ATGTACCAAGTGTCCCAAGAAATCCCTGTCTCCAGGAATGCAACTCCCAAGTTAAACA 477

Qy 500 CTGTGTGAGTTCATCTGTTTCAAGA 525

Db 478 CTGTGTGAGTTCATCTGTTTCAAA 503

RESULT 13
CN687949
LOCUS
DEFINITION E0250A07-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, high density) cDNA library (Long) Mus musculus cDNA clone NIA:E0250A07 IMAGE:30854118 5', mRNA sequence.

ACCESSION CN687949
VERSION 1
KEYWORDS GI:47454395
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y., VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L., Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.

TITLE Transcriptome analysis of mouse stem cells and early embryos
JOURNAL PLoS Biol. 1 (3), 410-419 (2003)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0250 row: A column: 07
Seq primer: M13 Reverse
High quality sequence stop: 614
POLYA=No.

FEATURES
source
1. .614
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/EvTac"
/db_xref="niaEST:E0250A07-5"
/db_xref="taxon:10090"
/clone="NIA:E0250A07 IMAGE:30854118"
/sex="Male"
/tissue_type="Embryonic Stem Cell"
/cell_line="129.3 ES cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, high density) cDNA library (Long)"
/note="vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]]. ES cells were plated at density 3x10⁴/cm², on gelatin-coated plates and cultured for 48 hrs at 37 °C, 5% CO₂. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine, 0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGAGCGCGCCCTTTT-3'] from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lona-linker Lu-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using

Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.4 kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 50.5%; Score 354.6; DB 7; Length 614;
Best Local Similarity 90.6%; Pred No. 1.4e-91;
Matches 378; Conservative 0; Mismatch 39; Indels 0; Gaps 0;

Qy 107 TGGCCTTGAGGTAAATTTGCTATGCTAGAAATACACTCTTCAATGTCGCGTGGT 166
Db 1 TGTCTTGGCGTAATATTGCTATGCTGCTGAATCATACTCTTCAACTGTCCGATGGT 60

Qy 167 AATACTGGTCTAAAGAGCTGTGTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCG 226
Db 61 AATACCAGTCTAATGATGTCTGTTGCAAGACCTGTCCCTCAGGTACATTTGTCAAGGCG 120

Qy 227 CTTGCCAAATCCCCCATCTCAAGGCAATGTGAGAAGTGTCAACCAAGGAACATTTACAG 286
Db 121 CTTGCAAAATCCCCCATCTCAAGGCAATGTGAGAAGTGTCAACCAAGGAACATTTACAG 180

Qy 287 AGAAAGATAATTAACCTGGATGCTTGTATCTTTGCTCCACCTGTGATAAAGATCAGAAA 346
Db 181 GGAAGATAATGCGCTGCATGATTGTGAACCTTTGCTCCACCTGTGATAAAGACAGAATA 240

Qy 347 TGTGCGCGACTCTCAGCCACAGTGACCGGAAATGCCAGTGCAGAACAGGCTTTTACT 406
Db 241 TGTGCGCTGACTCTTCTGCGCGCAGTGACCGGAAATGCCAGTGCAGAACAGGCTTACT 300

Qy 407 ACTATGACCCAAATTTCCAGAAATCGTCGCCCCCATGTACCAAGTGTCCCAAGGAATCC 466
Db 301 ACTATGACCCAAATTTCCGAAATCATGCGCCCATGTACCAAGTGTCCCAAGGAATCC 360

Qy 467 CTGTCCTCCAGGAATGCACTCCACAGCTAACACTGTGTGCAGTTTCATCTGTTTCAA 523
Db 361 CTGTCCTCCAGGAATGCACTCCACAGCTAACACTGTGTGCAGTTTCATCTGTTTCAA 417

RESULT 14

LOCUS CN697902
DEFINITION E0401A05-5 NIA Mouse E11.5 whole embryo cDNA library (Long) Mus musculus cDNA clone NIA:E0401A05 IMAGE:30868612 5', mRNA sequence.

ACCESSION CN697902
VERSION 1
KEYWORDS GI:47466651
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y., VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L., Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.

TITLE Transcriptome analysis of mouse stem cells and early embryos
JOURNAL PLoS Biol. 1 (3), 410-419 (2003)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0401 row: A column: 05
Seq primer: M13 Reverse

High quality sequence stop: 597

POLYA=No.

FEATURES

source

Location/Qualifiers

1..597

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="niaEST:E0401A05-5"

/db_xref="taxon:10090"

/clone="NIA:E0401A05 IMAGE:30868612"

/tissue type="whole embryo including extraembryonic

tissues at 11.5-days postcoitum"

/dev_stage="E11.5"

/lab_host="DH10B"

/clone_lib="NIA Mouse E11.5 whole embryo cDNA library

(long)"

/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://igsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 3 embryos at 11.5-days postcoitum. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen]: 5'-pGACTAGTCTAGATCGGAGCGGCCCTTTTTTTTTTTT-3' from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lona-linker Lu-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.3Kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match	50.4%;	Score 353.6;	DB 7;	Length 597;
Best Local Similarity	91.7%;	Pred. No. 2.8e-91;	Mismatches 34;	Indels 0; Gaps 0;
Matches 374;	Conservative 0;			

QY	116	AGGTAATAATTTGCTATGCTAGAAATACACTCTCTCAAAATGTCGCTGGTGAATACGTGT	175
Db	97	AGGTAATAATTTGCTATGCTAGAAATACACTCTCTCAAAATGTCGCTGGTGAATACGTGT	156
QY	176	CTAAAGAGCTGTGTTGCAAGAACTGTTCTGAGAGTACATTTGTCAAGCGCCCTGCGAAA	235
Db	157	CTAATGATGCTGTGTTGCAAGAACTGTCGCTCAGGTACATTTGTCAAGCGCCCTGCAAAA	216
QY	236	TCCCCATACCTCAAGGAAATGTGAGAGTGTACCCAGGAGACATTCACAGAGAAAGATA	295
Db	217	TCCCCATACCTCAAGGAAATGTGAGAGTGTACCCAGGAGACATTCACAGGAAAGATA	276
QY	296	ATTACTCGATGCTTGTATCTTTCTCCACTGTGATAAAGATCAGGAAATGTGGCGCG	355
Db	277	ATGCGCTGATGATTTGTGACTTTTCTCCACTGTGATAAAGATCAGGAAATGTGGCGCG	336
QY	336	ACTGCTAGCCACAGTACCGGAAATGCGAGTGCAGAGTCTTTACTACTATGACC	415
Db	337	ACTGTTCTGCCACAGTACCGGAAATGCGAGTGCAGAGTCTTTACTACTATGACC	396
QY	416	CAAAATTTCCAGAACTGTCGCGCCCATGTACCAAGTGTCCCAAGGAATCCTGTCCTCC	475
Db	397	CAAAATTTCCAGAACTGTCGCGCCCATGTACCAAGTGTCCCAAGGAATCCTGTCCTCC	456
QY	476	AGGAATGCAACTCCACAGTAACTAGTGTGAGTTCATCTGTTTCAA	523
Db	457	AGGAATGCAACTCCACAGTAACTAGTGTGAGTTCATCTGTTTCAA	504

RESULT 15

BY182663

LOCUS

DEFINITION

371 bp mRNA linear EST 10-DEC-2002

BY182663 RIKEN full-length enriched, NOD-derived CD11c +ve

dendritic cells Mus musculus cDNA clone F630103C16 5', mRNA

sequence.

BY182663

VERSION

BY182663.1

GI:26319309

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 371)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yananaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,

Clothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Guinichich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Kongsawa, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verardo, R., Wagner, L., Walested, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itch, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>

Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-Format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2005, 07:09:19 ; Search time 116.19 Seconds
(without alignments)
115.645 Million cell updates/sec

Title: US-10-622-407-10

Perfect score:

Sequence: 1 MFGFFCCLVSSLSRWFLWRR.....ANTVCSSSVSRRSASVAWPI 180

Scoring table: BLOSUM62

Learning curve: 200000
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

[illegible]

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2 6/ptodata/1/iaa/6A_COMB.pcp:*

```
4: /cgn2_6/ptodata/1/1aa/6B COMB.pcp:
5: /cgn2_6/ptodata/1/1aa/6B COMB.pcp:
```

```
5: /eghz_6/ptodata/1/1aa/PC1US COMB.pesl nesl
6: /cqn2_6/ntodata/1/1aa/backf1.esl nesl
```

o: /cgnz_v/prodata/r/1aa/pack11111111:pr

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1008	100.0	180	4	US-09-612-033B-10	Sequence 10, Appl	
2	956	94.8	198	4	US-09-612-033B-8	Sequence 8, Appl	
3	956	94.8	138	4	US-09-612-033B-14	Sequence 14, Appl	
4	748	74.2	133	4	US-09-612-033B-6	Sequence 6, Appl	
5	705	69.9	176	3	US-09-411-722-1	Sequence 1, Appl	
6	705	69.9	176	4	US-09-855-266A-1	Sequence 1, Appl	
7	641	63.6	148	3	US-09-611-722-2	Sequence 2, Appl	
8	641	63.6	148	4	US-09-855-266A-2	Sequence 2, Appl	
9	212.5	21.1	123	4	US-09-855-266A-13	Sequence 13, Appl	
10	208.5	20.7	355	1	US-08-292-549-6	Sequence 6, Appl	
11	208.5	20.7	355	3	US-09-006-353A-14	Sequence 14, Appl	
12	208.5	20.7	355	4	US-09-573-986-14	Sequence 14, Appl	
13	207.5	20.6	285	3	US-08-804-166-6	Sequence 6, Appl	
14	207.5	20.6	285	3	US-08-910-991-6	Sequence 6, Appl	
15	207.5	20.6	285	4	US-09-756-186-6	Sequence 6, Appl	
16	203.5	20.2	256	3	US-08-804-166-2	Sequence 2, Appl	
17	203.5	20.2	256	3	US-08-910-991-2	Sequence 2, Appl	
18	203.5	20.2	256	4	US-09-756-186-2	Sequence 2, Appl	
19	203.5	20.2	307	3	US-08-804-166-4	Sequence 4, Appl	
20	203.5	20.2	307	3	US-08-910-991-4	Sequence 4, Appl	
21	203.5	20.2	307	4	US-09-756-186-4	Sequence 4, Appl	
22	203.5	20.2	336	3	US-08-804-166-8	Sequence 8, Appl	
23	203.5	20.2	336	3	US-08-910-991-8	Sequence 8, Appl	
24	203.5	20.2	336	4	US-09-756-186-8	Sequence 8, Appl	
25	202.5	20.1	199	1	US-08-050-319B-48	Sequence 48, Appl	
26	202.5	20.1	199	2	US-08-465-982-48	Sequence 48, Appl	
27	201.5	20.0	167	1	US-08-050-319B-2	Sequence 2, Appl	

```
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-612-033B-8

Query Match          94.8%; Score 956; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 6.9e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQDMVADCSATS 120
Db 61 KNCAGTFVAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQDMVADCSATS 120

Qy 121 DRKQCQRTGLYYDPKPEPCRPCTKCPQGIPLVQECNSTANTVCCSSVS 170
Db 121 DRKQCQRTGLYYDPKPEPCRPCTKCPQGIPLVQECNSTANTVCCSSVS 170

RESULT 3
US-09-612-033B-14
; Sequence 14, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmat2, a No. 6627199el Member of the TNF-Receptor Superfamily
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: immunoglobulin sequences
US-09-612-033B-14

Query Match          94.8%; Score 956; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQDMVADCSATS 120
Db 61 KNCAGTFVAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQDMVADCSATS 120

Qy 121 DRKQCQRTGLYYDPKPEPCRPCTKCPQGIPLVQECNSTANTVCCSSVS 170
Db 121 DRKQCQRTGLYYDPKPEPCRPCTKCPQGIPLVQECNSTANTVCCSSVS 170

RESULT 4
US-09-612-033B-6
```

```
; Sequence 6, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmat2, a No. 6627199el Member of the TNF-Receptor Superfamily
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-612-033B-6

Query Match          74.2%; Score 748; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.1e-63;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQDMVADCSATS 120
Db 61 KNCAGTFVAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQDMVADCSATS 120

Qy 121 DRKQCQRTGLYY 133
Db 121 DRKQCQRTGLYY 133

RESULT 5
US-09-411-722-1
; Sequence 1, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501/040001
; CURRENT APPLICATION NUMBER: US/09/411,722
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-1

Query Match          69.9%; Score 705; DB 3; Length 176;
Best Local Similarity 79.9%; Pred. No. 3.3e-59;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

Qy 7 SLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCSAG 66
Db 5 SHVSSLSHWF-----LLLLLLLLLPLVIFAMPESYSEFCPDGGEYQSDNDVCCCTCPG 56

Qy 67 TFVKAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQDMVADCSATSDRKQC 126
Db 57 TFVKAPCKIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQDMVADCSATSDRKCEC 116

Qy 127 RTGLYYDPKPEPCRPCTKCPQGIPLVQECNSTANTVCCSSVS 170
```

```

Db      117 QIGLYYDYPKPPESCRPTKCPQIGIPVLQECNNTANTVCSSVS 160
: |||||
RESULT 6
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-1

Query Match      69.9%; Score 705; DB 4; Length 176;
Best Local Similarity 79.9%; Pred. No. 3.1e-59;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY      7 SLVSSSRWFLRRLLLLLLLLLLNLPLQVKFAMLEHSPKCPAGEYWSKDVCKKNCAG 66
: |||||
Db      5 SHVSSLSHWF-----L L L L L L L L F L P I F A M P E S I F N C P D G E T Q S N D V C K T C P S G 56
: |||||

QY      67 TFVKAPCEIPTHQOCEKCHPGFTTEKDNLYDACLSTCDKQDMVADCSATSDRKQC 126
: |||||
Db      57 TFVKAPCKIPTHQOCEKCHPGFTTGKNGLHDCELSTCDKQDMVADCSATSDRKCEC 116
: |||||

QY      127 RTGLYYDYPKPPESCRPTKCPQIGIPVLQECNNTANTVCSSVS 170
: |||||
Db      117 QIGLYYDYPKPPESCRPTKCPQIGIPVLQECNNTANTVCSSVS 160
: |||||

RESULT 7
US-09-411-722-2
; Sequence 2, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501/040001
; CURRENT APPLICATION NUMBER: US/09/411,722
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-2

Query Match      63.6%; Score 641; DB 3; Length 148;
Best Local Similarity 84.8%; Pred. No. 3.1e-53;
Matches 112; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY      39 AMLEHSPKCPAGEYWSKDVCKKNCAGTFVKAPCEIPTHQOCEKCHPGFTTEKDNLYD 98
: |||||
Db      1 AMPEYSYFNCPDGEYQSDVCKTCPSGTFVKAPCKIPTHQOCEKCHPGFTTGKDNGLH 60
: |||||

QY      99 ACILSTCDKQDMVADCSATSDRKQCQRTGLYYDYPKPPESCRPTKCPQIGIPVLQECN 158
: |||||
Db      61 DCELCSTCDKQDMVADCSATSDRKCECQIGLYYDYPKPPESCRPTKCPQIGIPVLQECN 120
: |||||

QY      159 STANTVCSSVS 170
: |||||
Db      121 STANTVCSSVS 132
: |||||

RESULT 8
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-2

Query Match      63.6%; Score 641; DB 4; Length 148;
Best Local Similarity 84.8%; Pred. No. 3.1e-53;
Matches 112; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY      39 AMLEHSPKCPAGEYWSKDVCKKNCAGTFVKAPCEIPTHQOCEKCHPGFTTEKDNLYD 98
: |||||
Db      1 AMPEYSYFNCPDGEYQSDVCKTCPSGTFVKAPCKIPTHQOCEKCHPGFTTGKDNGLH 60
: |||||

QY      99 ACILSTCDKQDMVADCSATSDRKQCQRTGLYYDYPKPPESCRPTKCPQIGIPVLQECN 158
: |||||
Db      61 DCELCSTCDKQDMVADCSATSDRKCECQIGLYYDYPKPPESCRPTKCPQIGIPVLQECN 120
: |||||

QY      159 STANTVCSSVS 170
: |||||
Db      121 STANTVCSSVS 132
: |||||

RESULT 9
US-09-855-266A-13
; Sequence 13, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; 
```


Query Match 20.6%; Score 207.5; DB 3; Length 285;

```

133 YDPKPPBSCRCTKCPGIPVLOECNSTANTVCS 166
      :      |      |      |      |
117 YWSENLFCQFNCTLCNG-TVHLSQSQKQNTVCT 149

```

Search completed: September 9, 2005, 09:35:54
Job time : 117.19 secs

Search completed: September 9, 2005, 09:35:54
Job time : 117.19 secs

Query Match	20.6%	Score 207.5;	DB 4;	Length 285;
Best Local Similarity	34.4%;	Pred. No. 6.3e-12;		
Matches	53;	Conservative 17;	Mismatches 71;	Indels 13; Gaps 6;

QY	20	RLLLLLLLLLLLP-LQVFMLELHSHFKPAGEY---	WSKVCCNCSAGTFVKAPCEI	75
Db	2	RTSLILAFGLLCLPWLQESA-----DSVCPQKGIHPQNNISCTCKHKGTYLYND	CPG	56
QY	76	PHTQGCCKHCPGTFTEKQNYLDACILCSTDKD--QEWVADCSATSDRCQCRGTGLY-Y	132	
Db	57	PGQDTCRCESGSGFTASENHLRHLCSSKCRKEMGQVEISSCTVDRTDTCGCRKNQYRH	116	

	Query Match	Best Local Similarity	Score	DB 15;	Length	DB 180;
	Matches	Conservative	Mismatches	Indels	Gaps	
Qy	1	100.0%;	100.0%;	0;	0;	0;
Db	1	100.0%;	100.0%;	0;	0;	0;
Qy	61	100.0%;	100.0%;	0;	0;	0;
Db	61	100.0%;	100.0%;	0;	0;	0;

Qy 121 DRKQCRRTGLYYDPKPEPCRCPTKCPQGIPLVQECNSTANTVCSSSVSRSSASVAVPI 180
Db 121 DRKQCRRTGLYYDPKPEPCRCPTKCPQGIPLVQECNSTANTVCSSSVSRSSASVAVPI 180

RESULT 2

US-10-622-407-8
; Sequence 8, Application US/10622407
; Publication No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US/10/622.407
; CURRENT FILING DATE: 2003-07-17
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/612,033
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-622-407-8

Query Match 94.8%; Score 956; DB 15; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.5e-76;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILSTCDKQEMVADCSATS 120

Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILSTCDKQEMVADCSATS 120

Qy 121 DRKQCRRTGLYYDPKPEPCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170

Db 121 DRKQCRRTGLYYDPKPEPCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170

RESULT 3

US-10-622-407-14
; Sequence 14, Application US/10622407
; Publication No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US/10/622.407
; CURRENT FILING DATE: 2003-07-17
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/612,033
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: immunoglobulin sequences
US-10-622-407-14

Query Match 94.8%; Score 956; DB 15; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.9e-76;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILSTCDKQEMVADCSATS 120
Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILSTCDKQEMVADCSATS 120
Qy 121 DRKQCRRTGLYYDPKPEPCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170
Db 121 DRKQCRRTGLYYDPKPEPCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170

RESULT 4

US-10-622-407-6
; Sequence 6, Application US/10622407
; Publication No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US/10/622.407
; CURRENT FILING DATE: 2003-07-17
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/612,033
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-622-407-6

Query Match 74.2%; Score 748; DB 15; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILSTCDKQEMVADCSATS 120

Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILSTCDKQEMVADCSATS 120

Qy 121 DRKQCRRTGLYY 133

Db 121 DRKQCRRTGLYY 133

RESULT 5

US-10-193-616-14
; Sequence 14, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07

```
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: ymkz5-Fc fusion protein
US-10-193-616-14

Query Match      70.3%; Score 709; DB 14; Length 396;
Best Local Similarity 78.6%; Pred. No. 2.8e-54;
Matches 132; Conservative 6; Mismatches 22; Indels 8; Gaps 1;

QY 7 SLVSSLSRWFLWRLRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVCCNCSAG 66
DB 5 SHVSSLSHWP-----LRLRLRLPLVPVIFAMPESYFNCNCPDGEYQSNVCCNCPG 56

QY 67 TFVKAPCEIPHTQOCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPESCRCPTKCPQIPVLQECNNTANTVCSSSVSRSA 174
DB 117 QIGLYYYDDPKFPESCRCPTKCPQIPVLQECNNTANTVCSSSVSNAAA 164

RESULT 6
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; PRIOR FILING DATE: 2001-05-14
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-1

Query Match      69.9%; Score 705; DB 9; Length 176;
Best Local Similarity 79.9%; Pred. No. 2.9e-54;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY 7 SLVSSLSRWFLWRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVCCNCSAG 66
DB 5 SHVSSLSHWP-----LRLRLRLPLVPVIFAMPESYFNCNCPDGEYQSNVCCNCPG 56

QY 67 TFVKAPCEIPHTQOCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPESCRCPTKCPQIPVLQECNNTANTVCSSSVS 170
DB 117 QIGLYYYDDPKFPESCRCPTKCPQIPVLQECNNTANTVCSSSVS 160

RESULT 7
US-10-193-616-8
; Sequence 8, Application US/10193616
; Publication No. US20030096355A1

; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-193-616-8

Query Match      69.9%; Score 705; DB 14; Length 176;
Best Local Similarity 79.9%; Pred. No. 2.9e-54;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY 7 SLVSSLSRWFLWRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVCCNCSAG 66
DB 5 SHVSSLSHWP-----LRLRLRLPLVPVIFAMPESYFNCNCPDGEYQSNVCCNCPG 56

QY 67 TFVKAPCEIPHTQOCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPESCRCPTKCPQIPVLQECNNTANTVCSSSVS 170
DB 117 QIGLYYYDDPKFPESCRCPTKCPQIPVLQECNNTANTVCSSSVS 160

RESULT 8
US-10-802-332-1
; Sequence 1, Application US/10802332
; Publication No. US20040152879A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/10/802,332
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: US/09/855,266
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-802-332-1

Query Match      69.9%; Score 705; DB 16; Length 176;
Best Local Similarity 79.9%; Pred. No. 2.9e-54;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY 7 SLVSSLSRWFLWRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVCCNCSAG 66
DB 5 SHVSSLSHWP-----LRLRLRLPLVPVIFAMPESYFNCNCPDGEYQSNVCCNCPG 56

QY 67 TFVKAPCEIPHTQOCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPESCRCPTKCPQIPVLQECNNTANTVCSSSVS 170
DB 117 QIGLYYYDDPKFPESCRCPTKCPQIPVLQECNNTANTVCSSSVS 160
```

Db	57	TFVAPKPIPTQGOCEKHPGTFTGKNGLHDCELGCTCDKQNVVDCSATSDRKCC	116
Qy	127	RTGLYYYPDKPPESCRCTCKPGIPLVQECNSTANTVCSSSVS	170
Db	117	QIGLYYYPDKPPESCRCTCKPGIPLVQECNSTANTVCSSSVS	160

```

RESULT 9
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-2

```

Query Match	63.6%;	Score 641;	DB 9;	Length 148;
Best Local Similarity	84.8%;	Pred. No. 1.1e-48;		
Matches 112;	Conservative 5;	Mismatches 15;	Indels 0;	Gaps 0;
Qy	39	AMLELHSPKCPAGEYWSKDVCCKNSAGTFVKAPCEIPIHTQGOCEKCHGPTTEKDNYLD	98	
Db	1	AMPEYSFNCPPGEYQSDNVCCKTPSGGTFVKAPCKIPIHTQGOCEKCHGPTFGKDNGLH	60	
Qy	99	ACILGTCDCDKQEMWADCSATSDRKCOCRTGLYYDPKFPESCRTCTKCPQGIPIVLQECN	158	
Db	61	DCELSTCDKQNMWADCSATSDRKCBCQGLYYDPKFPESCRTCTKCPQGIPIVLQECN	120	
Qy	159	STANTVTCSSVS	170	
Db	121	STANTVTCSSVS	132	

```

RESULT 10
US-10-802-332-2
; Sequence 2, Application US/10802332
; Publication NO. US20040152879A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/10/802,332
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: US/09/855,266
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148

```

```

Qy 7 SLVSSLSRWFMLRRLLLLLLLLLLNLPLQVKFAMLELHSPKPAGEYWKDVCCNCSAG 66
Db 5 SHVSSLSHWF-----LLLLLLNLFLPVIFAMPESYFNCPDGEYQSNVDVCKTCPSG 56
Qy 67 TFWKAPCEIPIHTQOCBKCHPGTFTFXDNVLDACILCTCDKQDMVADCSATSDRKQC 126
Db 57 TFWKAPCKIPIHTQOCBKCHPGTFTGXDNGLHDCELCSTCDKQDMVADCSATSDRKQC 116
Qy 127 R 127
Db 117 Q 117

RESULT 12
US-10-193-616-10
; Sequence 10, Application US/10193616
; Publication No. US2003009635A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193.616

```

```
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: TNFRI
US-10-193-616-10

Query Match      21.6%; Score 217.5; DB 14; Length 247;
Best Local Similarity 32.3%; Pred. No. 3.6e-11;
Matches 51; Conservative 19; Mismatches 75; Indels 13; Gaps 5;

QY 21 LLLLLLLLLLNL-----PLQVXFAMLELHSPKCPAGEY---WSKDVCCCKNSAGTFVKA 71
DB 11 LSLVLLALLMGHPSGVTGLVPSLGDREKRDLSLCPQGYVHSKNSICCTKCHKGTLYVS 70

QY 72 PCBIPTQGOCEKCHPGTFTTEKDYLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
DB 71 DCPSGRDVTVCRECEKGTFTTASQNYLRQCLSCCTCKEMSQVETSPQADKDTVCGCKEN 130

QY 130 LYY-YDPKFPESCRCPTCKPQGIPLVQECNSTANTVCS 166
DB 131 QFORYLSETHFCVDCSPCFNG-TVTIPCKETQNTVCN 167

RESULT 13
US-10-410-012-3
; Sequence 3, Application US/10410012
; Publication No. US20030228276A1
; GENERAL INFORMATION:
; APPLICANT: Pitossi, Fernando J
; APPLICANT: Eisell, Ulrich L M
; TITLE OF INVENTION: Neuroprotective and neurodegenerative effects of long-term expres
; FILE REFERENCE: 1418P US/101141-17
; CURRENT APPLICATION NUMBER: US/10/410,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/370,974
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 3
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-012-3

Query Match      21.6%; Score 217.5; DB 15; Length 454;
Best Local Similarity 32.3%; Pred. No. 6.5e-11;
Matches 51; Conservative 19; Mismatches 75; Indels 13; Gaps 5;

QY 21 LLLLLLLLLLNL-----PLQVXFAMLELHSPKCPAGEY---WSKDVCCCKNSAGTFVKA 71
DB 11 LSLVLLALLMGHPSGVTGLVPSLGDREKRDLSLCPQGYVHSKNSICCTKCHKGTLYVS 70

QY 72 PCBIPTQGOCEKCHPGTFTTEKDYLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
DB 71 DCPSGRDVTVCRECEKGTFTTASQNYLRQCLSCCTCKEMSQVETSPQADKDTVCGCKEN 130

QY 130 LYY-YDPKFPESCRCPTCKPQGIPLVQECNSTANTVCS 166
DB 131 QFORYLSETHFCVDCSPCFNG-TVTIPCKETQNTVCN 167

RESULT 14
US-10-799-345-24
```

```
; Sequence 24, Application US/10799345
; Publication No. US20040209316A1
; GENERAL INFORMATION:
; APPLICANT: Christopher T. Ritchlin
; APPLICANT: Sally Haas-Smith
; APPLICANT: Edward Schwarz
; TITLE OF INVENTION: Methods and Compositions Related to
; TITLE OF INVENTION: Joint Inflammation Diseases
; FILE REFERENCE: 21108.003102
; CURRENT APPLICATION NUMBER: US/10/799,345
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/454,573
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-799-345-24

Query Match      21.6%; Score 217.5; DB 16; Length 454;
Best Local Similarity 32.3%; Pred. No. 6.5e-11;
Matches 51; Conservative 19; Mismatches 75; Indels 13; Gaps 5;

QY 21 LLLLLLLLLLNL-----PLQVXFAMLELHSPKCPAGEY---WSKDVCCCKNSAGTFVKA 71
DB 11 LSLVLLALLMGHPSGVTGLVPSLGDREKRDLSLCPQGYVHSKNSICCTKCHKGTLYVS 70

QY 72 PCBIPTQGOCEKCHPGTFTTEKDYLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
DB 71 DCPSGRDVTVCRECEKGTFTTASQNYLRQCLSCCTCKEMSQVETSPQADKDTVCGCKEN 130

QY 130 LYY-YDPKFPESCRCPTCKPQGIPLVQECNSTANTVCS 166
DB 131 QFORYLSETHFCVDCSPCFNG-TVTIPCKETQNTVCN 167

RESULT 15
US-09-855-266A-13
; Sequence 13, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-13

Query Match      21.1%; Score 212.5; DB 9; Length 123;
Best Local Similarity 34.7%; Pred. No. 5e-11;
Matches 43; Conservative 15; Mismatches 59; Indels 7; Gaps 4;

QY 48 CPAGEY---WSKDVCCCKNSAGTFVKAPEIPTQGOCEKCHPGTFTTEKDYLDACILCS 104
DB 1 CPGGYVHSKNSICCTKCHKGTLYVSDCPSGRDVTVCRECEKGTFTTASQNYLRQCLSC 60
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2005, 06:50:20 ; Search time 130.476 Seconds
(without alignments)
132.737 Million cell updates/sec

Title: US-10-622-407-10

Perfect score: 1008

Sequence: 1 MFGFFCSLVSLSRWFLMR.....ANTVCSVVSRSSASVAMPI 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217.5	21.6	454	1 GQMTT1	tumor necrosis fac
2	204.5	20.3	461	1 GQRTT1	tumor necrosis fac
3	201.5	20.0	348	2 T28623	hypothetical prote
4	201.5	20.0	349	2 D36858	gene G4R protein -
5	201.5	20.0	349	2 D72175	G2R protein - vari
6	201.5	20.0	455	1 GQHUT1	tumor necrosis fac
7	200.5	19.9	461	2 JC4302	tumor necrosis fac
8	188	18.7	271	2 S12783	OX40 antigen precu
9	188	18.7	324	2 JC2395	Fas antigen precu
10	188	18.7	427	1 GQHUN	nerve growth facto
11	183	18.2	327	2 A46484	apoptosis-mediatin
12	182	18.1	314	2 I37383	FAS soluble protei
13	180.5	17.9	651	2 JC7705	death receptor-6 -
14	180	17.9	335	2 A40036	apoptosis-mediatin
15	176.5	17.5	416	1 JN0006	nerve growth facto
16	175	17.4	425	1 A26431	nerve growth facto
17	173.5	17.2	461	1 A35356	tumor necrosis fac
18	173	17.2	325	2 A43692	T2 protein - rabbi
19	167.5	16.6	326	1 GQVZML	T2 protein - myxom
20	163.5	16.2	272	2 I48700	gene OX40 protein
21	157.5	15.6	260	1 I48700	CD27 antigen precu
22	154.5	15.3	474	2 B38634	tumor necrosis fac
23	150	14.9	459	2 I48854	gene murine tumour
24	150	14.9	595	2 A42086	CD30 antigen precu
25	149.5	14.8	250	1 A49053	CD27 antigen precu
26	149.5	14.8	435	2 I54182	tumor necrosis fac
27	143	14.2	277	2 I37552	OX40 homolog - hum
28	126	12.5	1790	1 MWFFB1	laminin beta-1 cha
29	122	12.1	305	2 A46476	B cell-associated

30	121	12.0	493	2 JC5486	membrane glycoprot
31	119	11.8	255	2 I38426	lymphocyte activat
32	119	11.8	3635	2 T10053	laminin alpha 5 ch
33	118	11.7	4391	2 A38096	perlecan precursor
34	115.5	11.5	713	2 A35502	major surface-labe
35	115	11.4	256	2 B32393	T-cell antigen 4-1
36	115	11.4	557	2 A48434	variant-specific s
37	114.5	11.4	1193	2 A44018	laminin B2t chain
38	114	11.3	1339	2 JC4387	epidermal growth f
39	113	11.2	1827	2 T34288	hypothetical prote
40	112.5	11.2	667	2 A48579	trophozoite surfac
41	112.5	11.2	1609	1 MWHUB2	laminin gamma-1 ch
42	112	11.1	3707	2 S18252	heparan sulfate pr
43	111.5	11.1	1801	1 MMRIS	laminin beta-2 cha
44	111	11.0	1548	2 S34583	serine proteinase
45	110	10.9	1192	2 S69000	laminin gamma 2 ch

ALIGNMENTS

RESULT 1

GQMTT1

tumor necrosis factor receptor 1 precursor - mouse

N;Alternate names: tumor necrosis factor receptor, 55K

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004

C;Accession: A38634; B40254; S16677; S19021; I54532; I57826

R;Lewis, M.; Tagaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r

A;Reference number: A38634; MUID:91187885; PMID:1849278

A;Accession: A38634

A;Molecule type: mRNA

A;Residues: 1-454 <EW>

A;Cross-references: UNIPROT:P25118; GB:M60468; NID:9199825; PIDN:AAA39751.1; PID:9199826

R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk

Mol. Cell. Biol. 11, 3020-3026, 1991

A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A;Reference number: A40254; MUID:91246168; PMID:1645445

A;Accession: B40254

A;Molecule type: mRNA

A;Residues: 1-454 <GO2>

A;Cross-references: GB:M60468; NID:9199825; PIDN:AAA39751.1; PID:9199826

R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissenerghis, A.M.; Gray, P.W.; Feldma

Eur. J. Immunol. 21, 1649-1656, 1991

A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis

A;Reference number: S16677; MUID:91285014; PMID:1647956

A;Accession: S16677

A;Molecule type: mRNA

A;Residues: 1-454 <BAR>

A;Cross-references: EMBL:X59238; NID:953578; PIDN:CAA41922.1; PID:953579

R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.

Immunogenetics 34, 338-340, 1991

A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.

A;Reference number: S19021; MUID:92039815; PMID:1657766

A;Accession: S19021

A;Molecule type: mRNA

A;Residues: 1-454 <ROT>

A;Cross-references: EMBL:X57796; NID:954848; PIDN:CAA40936.1; PID:954849

R;Bebo, B.F.

Immunogenetics 39, 450-451, 1994

A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1

A;Reference number: I54532; MUID:94245292; PMID:8188324

A;Accession: I54532

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-454 <RES>

A;Cross-references: GB:I26349; NID:9430732; PIDN:AAA59361.1; PID:9430733

R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.

Mol. Immunol. 30, 165-176, 1993

A;Title: Genomic organization and promoter function of the murine tumor necrosis factor

A;Reference number: I57826; MUID:93156721; PMID:8381516

A;Accession: I57826

tumor necrosis factor receptor 1 precursor [validated] - human

N/Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1

N/Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004

C/Accession: A38208, A34899, A34900; A36555; C36555; A36281; S12057; J70758; A60231; A38208

R/Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F. Genomics 13, 219-224, 1992

A/Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to chromosome 13

A/Reference number: A38208; MUID:92250049; PMID:1315717

A/Accession: A38208

A/Molecule type: DNA

A/Residues: 1-455 <FUC>

A/Cross-references: UNIPROT:P19438; GB:M75864; GB:M75865; GB:M75866; NID:G339748; PIDN:A38208

R/Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Leselaucher, C. Cell 61, 351-359, 1990

A/Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor

A/Reference number: A34899; MUID:90235284; PMID:2158862

A/Accession: A34899

A/Molecule type: mRNA

A/Residues: 1-455 <LOE>

A/Cross-references: GB:M58286; GB:M33480; NID:G339753; PIDN:AAA36753.1; PID:G339754

A/Experimental source: Placenta

A/Note: part of this sequence, including the amino end of the mature protein, confirmed by R/Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T. Cell 61, 361-370, 1990

A/Title: Molecular cloning and expression of a receptor for human tumor necrosis factor

A/Reference number: A34900; MUID:90235285; PMID:2158863

A/Accession: A34900

A/Molecule type: mRNA

A/Residues: 1-455 <SCH>

A/Cross-references: GB:M33294; NID:G339744; PIDN:AAA03210.1; PID:G339745

R/Himmler, A.; Maures-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; T. DNA Cell Biol. 9, 705-715, 1990

A/Title: Molecular cloning and expression of human and rat tumor necrosis factor receptors

A/Reference number: A36555; MUID:91090841; PMID:1702293

A/Accession: A36555

A/Molecule type: mRNA

A/Residues: 1-455 <HIM>

A/Cross-references: GB:M63121; NID:G339755; PIDN:AAA36754.1; PID:G339756

A/Accession: C36555

A/Molecule type: protein

A/Residues: 30-38/41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104, 107-128; 162-167, 'X', 169-210

A/Note: the purified protein, called tumor necrosis factor binding protein, is a soluble

R/Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M. Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990

A/Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re

A/Reference number: A38281; MUID:91017509; PMID:2170974

A/Accession: A38281

A/Molecule type: mRNA

A/Residues: 1-455 <GRA>

A/Cross-references: GB:M37764

A/Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372

R/Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann EMBO J. 9, 3269-3278, 1990

A/Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I form of the receptor.

A/Reference number: S12057; MUID:91006021; PMID:1698610

A/Accession: S12057

A/Molecule type: mRNA

A/Residues: 1-455 <NOP>

A/Cross-references: EMBL:X5313; NID:G37223; PIDN:CAA39021.1; PID:G37224

A/Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w

R/Kemper, O.; Wallach, D. Gene 134, 209-216, 1993

A/Title: Cloning and partial characterization of the promoter for the human p55 tumor ne

A/Reference number: J70758; MUID:94085779; PMID:8262379

A/Accession: J70758

A/Molecule type: DNA

A/Residues: 1-13 <KEM>

R/Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M. Eur. J. Immunol. 20, 1167-1174, 1990

A/Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence

RESULT 7

JC4302

tumor necrosis factor receptor p55 precursor - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C;Accession: JC4302; PC4093

R;Suter, B.; Pauli, U.

Gene 163, 263-266, 1995

A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

A;Reference number: JC4302; MUID:96011645; PMID:7590278

A;Accession: JC4302

A;Molecule type: mRNA

A;Residues: 1-461 <SUT>

A;Cross-references: UNIPROT:P50555; GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g11

A;Accession: PC4093

A;Molecule type: protein

A;Residues: 1-7 <SU2>

A;Experimental source: kidney cell line 15

C;Genetics:

C;Gene: tnfr

C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat hom

C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor

F;1-29/Domain: signal sequence #status predicted <SIG>

F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>

F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>

F;44-82/Domain: NGF receptor repeat homology <NG1>

F;84-126/Domain: NGF receptor repeat homology <NGF>

F;211-231/Domain: transmembrane #status predicted <TMM>

F;361-447/Domain: signal transduction #status predicted <SIT>

F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.9%; Score 200.5; DB 2; Length 461;

Best Local Similarity 30.8%; Pred. No. 4,9e-08;

Matches 49; Conservative 25; Mismatches 70; Indels 15; Gaps 7;

Qy 21 LLLLLLLLLLNL-PLOVKFAML-----ELHSFKCPAGEY---WSKDVCKKNSAGTFVKA 71

Db 11 LPVLRAALLVDVYPAGVGHGLVHLHPGDRERESLCPQGYKSHPNRSICCTKCHKGTYLHN 70

Qy 72 PCBIPTQCEKCHPGTFTEDKNYLDACILGTCG--DKDQEMVADCSATSDRKCCCRGTG 129

Db 71 DCLGPGLDTRCDRCNGTTFASENHLITQCLSCSKRSEMSQVEISPTVDRTVCGCRKN 130

Qy 130 LY--YYDKPPESCRPTCKPQIGIPVLQECNSTANTVCS 166

Db 131 QYRKWSETLFLQ-CLNCSLCPNG-TVQLPCLEKQDTICN 167

RESULT 8

SL2783

OX40 antigen precursor - rat

N;Alternate names: nerve growth factor receptor homolog

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: SL2783; S08036

R;Mallett, S.; Fossium, S.; Barclay, A.N.

EMBO J. 9, 1063-1068, 1990

A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc

A;Reference number: SL2783; MUID:90214614; PMID:2157591

A;Accession: SL2783

A;Molecule type: mRNA

A;Residues: 1-271 <MAL>

A;Cross-references: UNIPROT:P15725; EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57

C;Superfamily: CD27 antigen; NGF receptor repeat homology

C;Keywords: growth factor receptor; transmembrane protein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-271/Product: OX40 antigen #status predicted <MAT>

F;211-235/Domain: transmembrane #status predicted <TMM>

Query Match 18.7%; Score 188; DB 2; Length 271;

Best Local Similarity 27.1%; Pred. No. 2,9e-07;

```

Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor.
A;Reference number: A25218; MUID:87051725; PMID:3022937
A;Accession: A25218
A;Molecule type: mRNA
A;Residues: 1-427 <JOH>
A;Cross-references: UNIPROT:P08138; GB:M14764; NID:gl89204; PIDN:AAB59544.1; PID:gl89205
R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factor:
A;Reference number: A60204; MUID:87085574; PMID:3025363
A;Accession: A60204
A;Molecule type: protein
A;Residues: 29-31, 'T', 33-42, 'TT', 45-46, 'TX', 50-51, 'XX', 54-56 <MAR>
A;Experimental source: melanoma cell line A875
A;Note: This sequence has been corrected by a note added in proof to follow the nucleotide
R;Vissavajhala, P.; Leszyk, J.D.; Lin-Gosker, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor receptor
A;Reference number: S21689; MUID:92198017; PMID:1372492
A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
R;Shgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor
A;Reference number: I57638; MUID:89096903; PMID:2850481
A;Accession: I57638
A;Status: preliminary; translated from GB/EMBL/DBDJB
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: GB:W21621; NID:gl89206; PIDN:AAA36363.1; PID:gl89207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of the
C;Comment: This protein is thought to form a high-affinity receptor when it associates with
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDB:NGFR
A;Cross-references: GDB:I20234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NGI>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.7%; Score 188; DB 1; Length 427;
Best Local Similarity 34.7%; Pred. No. 4e-07;
Matches 50; Conservative 11; Mismatches 69; Indels 14; Gaps 5;

Qy 24 LLLLLLLNLP- QVKFAMLELHSPKAGEYWSKDVCKNCNSAGTVPKAPCEIPHTQGC 82
||||| : : : : : : : : : : : : : : : : : : : : : :
Db 15 LLLLLLLGVSLGGAKEA-----CPTGLYTHSECCACKNLGEGVAQPCGA--NOTVC 64
||||| : : : : : : : : : : : : : : : : : : : : : :

Qy 83 EKCHPG-TFTEKDNVLDACILCTCKDQEMVADCSATSDRKQCQRTGLVYYDPKPPESC 141
||||| : : : : : : : : : : : : : : : : : : : : : :
Db 65 EPLDSDVTFSVDVGATEPKCKTECVGLQSMSPCVCEADDAVCRCAYG--YYQDETGRC 122
||||| : : : : : : : : : : : : : : : : : : : : : :

Qy 142 RPCTKCPQGIPIVLQECNSTANTVC 165
||||| : : : : : : : : : : : : : : : : : : : : : :
Db 123 EACRVCEAGSLVTFSCQDKQNTVC 146
||||| : : : : : : : : : : : : : : : : : : : : : :

RESULT 11

```



```
F;141-181/Domain: NCG receptor repeat homology <NC4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      17.5%; Score 176.5; DB 1; Length 416;
Best Local Similarity 30.7%; Pred. No. 2.8e-06;
Matches 43; Conservative 20; Mismatches 68; Indels 9; Gaps 4;
```

Qy	27	L L A L N L P L Q V K F A M L E H S F K C P A G Y W S K D V C K N C S A G T F Y K A P C E I P H T O Q C E K C H	86
Dd	7	L L L L L L P A G T W S K E - - - - K C U T K M Y T T S G E C C K A C N L G E G V V Q P G V - - N Q T V C E P C L	60
Qy	87	P G - T F T E K N Y L D A C I L C S T C R D Q E M V A D C S A T S D R K C O C R T G L Y Y D P K F P E S C R P C T	145
Dd	61	D S V T Y S D T V S A T E P C K P C T C Q C V L G H S M S A P C V E S D D A V C R C A Y G - - Y F Q D E L S G S C K E C S	118
Qy	146	K C P Q G I P V L Q E C N S T A N T V C	165
Dd	119	I C E V G F G L M F P C R D S Q D T V C	138

Search completed: September 9, 2005, 09:31:39
Job time : 131.476 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 23:31:32 ; Search time 672.857 Seconds
(without alignments)
136.989 Million cell updates/sec

Title: US-10-622-407-10

Perfect score: 1008

Sequence: 1 MFQFCSLVSSLSRFLMRR.....ANTVCSSVSRRSASVAVPI 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	956	94.8	198	1 TR22 MOUSE	Q9er62 mus musculus
2	705	69.9	176	1 TR23 MOUSE	Q9er63 mus musculus
3	299	29.7	204	1 TR26 MOUSE	P83626 mus musculus
4	286.5	28.4	225	2 Q7T3M7	Q7t3m7 gallus gall
5	286.5	28.4	410	2 Q7T3M8	Q7t3m8 gallus gall
6	275.5	27.3	438	2 Q9DFV0	Q9dfv0 brachydanio
7	273.5	27.1	395	2 Q800K8	Q800k8 paralicthys
8	259	25.7	357	2 Q9DF34	Q9df34 brachydanio
9	249.5	24.8	321	2 Q6DJ81	Q6dj81 xenopus tro
10	249	24.7	328	2 Q76B99	Q76b99 xenopus lae
11	248	24.6	328	2 Q6GLZ4	Q6glz4 xenopus lae
12	239.5	23.8	289	2 Q678B7	Q678b7 lymphocysti
13	239	23.7	189	2 Q95185	Q95185 felis silve
14	233	23.1	446	2 Q95ND3	Q95nd3 felis silve
15	232	23.0	328	2 Q76B98	Q76b98 xenopus lae
16	221	21.9	347	2 Q57119	Q57119 cowpox viru
17	217.5	21.6	440	2 Q6QHF0	Q6qhf0 mus musculus
18	217.5	21.6	440	2 Q6QHF1	Q6qhf1 mus musculus
19	217.5	21.6	454	1 TR1A MOUSE	P25118 mus musculus
20	216	21.4	189	2 Q97530	Q97530 canis famil
21	215	21.4	360	2 Q57118	Q57118 cowpox viru
22	215.5	21.4	326	2 Q57120	Q57120 cowpox viru
23	215.5	21.4	348	2 Q57103	Q57103 monkeypox v
24	215.5	21.4	348	2 Q57108	Q57108 monkeypox v
25	215.5	21.4	348	2 Q57277	Q57277 monkeypox v
26	215.5	21.4	349	2 Q57107	Q57107 monkeypox v
27	215.5	21.4	349	2 Q57102	Q57102 monkeypox v
28	215.5	21.4	349	2 Q57291	Q57291 monkeypox v
29	215.5	21.4	349	2 Q57305	Q57305 cowpox viru
30	215.5	21.4	351	2 Q57121	Q57121 cowpox viru
31	215	21.3	323	1 TNR6_BOVIN	P51867 bos taurus

RESULT 1

ID	TR22_MOUSE	STANDARD;	PRT;	198 AA.
AC	Q9ER62; Q8VHB9; Q9CZA4;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DE	Tumor necrosis factor receptor superfamily member 22 (Tumor necrosis factor receptor p60 homolog 2) (TNF receptor family member SOBA)			
DE	(Decoy TRAIL receptor 2) (TNF receptor homolog 2)			
GN	Names=tnfrsf22; Synonyms=DcTrailr2, Tnfrh2, Tnfrsf1a2;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	STRAIN=129/SV; TISSUE=Embryonic stem cells;			
RX	MEDLINE=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691;			
RA	Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,			
RA	Lane N., Reik W., Walter J.;			
RT	"Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting."			
RL	Hum. Mol. Genet. 9:2691-2706(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND 3D-STRUCTURE			
RC	MODELING OF 62-170.			
RA	STRAIN=NIH Swiss;			
RX	PubMed=12466268; DOI=10.1074/jbc.M210783200;			
RA	Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A.,			
RA	Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,			
RA	Burkly L.C., Techoop J., Zheng T.S.;			
RT	"Identification of a new murine tumor necrosis factor receptor locus that contains two novel murine receptors for tumor necrosis factor-related apoptosis-inducing ligand (TRAIL)."			
RL	J. Biol. Chem. 278:5444-5454(2003).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Risser P., Mao W., Baldwin D.T., Pan G.;			
RT	"Characterization of SOBA, a murine member of the TNFR family."			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	STRAIN=C57BL/6J; TISSUE=Embryo;			
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;			
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,			
RA	Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,			
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrester A., Frazer K.S.,			
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,			

ALIGNMENTS

32	214.5	21.3	440	2	Q6QHF2
33	213.5	21.2	253	2	Q6WB14
34	213.5	21.2	326	2	O57122
35	213.5	21.2	351	1	CRMB COMPX
36	212.5	21.1	349	2	O57099
37	211.5	21.0	318	2	O7T2H3
38	211.5	21.0	332	1	TNR6_PIG
39	211	20.9	263	2	Q9XS60
40	211	20.9	319	2	Q9TV79
41	211	20.9	320	2	Q9XS29
42	210.5	20.9	347	2	O57115
43	209.5	20.8	349	1	CRMB CAMPS
44	209.5	20.8	349	2	O57098
45	209.5	20.8	349	2	O57100

Q6qhf2	mus	spretus
Q6wb14	callithrix	
O57122	cowpox viru	
O73559	cowpox viru	
O57099	monkeypox v	
O7t2h3	oncorhynch	
O7736	sus scrofa	
Q9xs60	oryctolagus	
Q9tv79	oryctolagus	
Q9xs29	oryctolagus	
O57115	cowpox viru	
O8uva7	camelopard	
O57098	camelopard	
O57100	monkeypox v	

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kogawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaezumi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Receptor for the cytotoxic ligand TNFSP10/TRAIL. Lacks a
CC cytoplasmic death domain and hence is not capable of inducing
CC apoptosis. Protects cells against TRAIL mediated apoptosis
CC possibly through ligand competition. Cannot induce the NF-kappa-B
CC pathway.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (isoform 1);
CC secreted (isoform 2) (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9ER62-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9ER62-2; Sequence=VSP_007648;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -!- CAUTION: Ref.1 (CAC27353) sequence differs from that shown due to
CC erroneous gene model prediction.
CC -!- CAUTION: Ref.1 (CAC16406) sequence differs from that shown due to
CC a frameshift in position 38.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; AJ278265; CAC16406.1; ALT_FRAME.
DR EMBL; AJ276505; CAC27353.1; ALT_SEQ.
DR EMBL; AY165626; AAN87806.1; -.
DR EMBL; AY165627; AAN87807.1; -.
DR EMBL; AY046551; AAL05073.1; -.
DR EMBL; AK012838; BAB28502.2; ALT_INIT.
DR HSSP; Q92956; LJWA.
DR MGD; MGI:1930270; Tnfrrsf22.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0004872; F:receptor activity; IDA.
DR GO; GO:0045569; F:TRAIL binding; IDA.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.
DR GO; GO:0042981; P:regulation of apoptosis; IDA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Alternative splicing; Glycoprotein; Receptor; Repeat; Signal-anchor;
KW Transmembrane.
FT DOMAIN 1 20 Cytoplasmic (Potential).
FT TRANSMEM 21 41 Signal-anchor for type II membrane
FT protein (Potential).
FT FT 42 198 Extracellular (Potential).
FT REPEAT 47 82 TNFR-Cys 1.

FT REPEAT 84 124 TNFR-Cys 2.
FT REPEAT 125 165 TNFR-Cys 3.
FT DISULFID 48 59 By similarity.
FT DISULFID 60 73 By similarity.
FT DISULFID 63 82 By similarity.
FT DISULFID 85 100 By similarity.
FT DISULFID 103 116 By similarity.
FT DISULFID 106 124 By similarity.
FT DISULFID 126 141 By similarity.
FT DISULFID 144 157 By similarity.
FT DISULFID 147 165 By similarity.
FT CARBOHYD 62 65 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 158 158 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 171 198 NPNRFLLLSPSLVSLVSVVVFRIIR -> RRSASVAVP
FT (in isoform 2).
FT FTID=VSP_007648.
FT L -> V (in Ref. 2).
FT L -> C (in Ref. 1; CAC16406).
FT LLLL -> CVV (in Ref. 1; CAC16406).
SQ SEQUENCE 198 AA; 23375 MW; EBF8F52961EA9983 CRC64;
Query Match 94.8%; Score 956; DB 1; Length 198;
Best Local Similarity 100.0%; Pred.No. 5.3e-75;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Qy 61 KNCAGTFVKAPEIPIHTQGCCKCHPGTFTKQNYLDACILGTCGDKQEMWADCSATS 120
Db 61 KNCAGTFVKAPEIPIHTQGCCKCHPGTFTKQNYLDACILGTCGDKQEMWADCSATS 120
Qy 121 DRKQCRTGLYYDPKPPESCPCPKCPQGPVLQECNSTANTVVCSSSVS 170
Db 121 DRKQCRTGLYYDPKPPESCPCPKCPQGPVLQECNSTANTVVCSSSVS 170
RESULT 2
TR23 MOUSE
ID TR23 MOUSE STANDARD; PRT; 176 AA.
AC Q9ER63; Q8VHC0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 23 precursor (Tumor
DE necrosis factor receptor p60 homolog 1) (TNF receptor family member
DE SOB) (Decoy TRAIL receptor 1) (TNF receptor homolog 1).
GN Name=Tnfrrsf23; Synonyms=Dctrailr1, Tnftr1, Tnfrrsf1all;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv; TISSUE=Embryonic stem cells;
RX MEDLINE=20519229; Pubmed=11063728; DOI=10.1093/hmg/9.18.2691;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region;
RT implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]
RP SEQUENCE FROM N.A.; FUNCTION, SUBCELLULAR LOCATION, AND 3D-STRUCTURE
RC MODELING OF 52-160.
RX STRAIN=C57BL/6;
RX Pubmed=12466268; DOI=10.1074/jbc.M210783200;
RA Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A.,
RA Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,
RA Burkly L.C., Tschopp J., Zheng T.S.;
RT "Identification of a new murine tumor necrosis factor receptor locus
RT that contains two novel murine receptors for tumor necrosis factor-
RT related apoptosis-inducing ligand (TRAIL).";


```

Qy 24 LLLLLLLNLPQVFKFAMLELHSPK-CPAGEYWSKDVCKKNCAGTFVKAPCEIPHTQGC 82
Db 4 LRLLLLLGLLRV--AVCSNITFLCKIGFPHKHNLCCLQCSAGTYLRNFCQENHNKSEC 61
Qy 83 EKCHPGFTFKDNYLDACILCTCDKQEMVADCSATSDRKQCQRTGLYYDPKFPESCR 142
Db 62 APCDSEHFIDHNKRESGFCPCVCRDDQEVAKSRTRADVQCCKQGTQYCDSENCLECH 121
Qy 143 PCTKCPGIPVLQECNSTANTVC 165
Db 122 TCSSCPDG-RVVRKCNATMDTVC 143

RESULT 4
Q7T3M7
ID Q7T3M7 PRELIMINARY; PRT; 225 AA.
AC Q7T3M7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Death domain-containing tumor necrosis factor receptor superfamily
DE member 23 variant 2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP BRIDGHAM J.T., JOHNSON A.L.;
RX PubMed=14645108;
RA "Bridgman J.T., Johnson A.L.;
RT "Alternatively spliced variants of Gallus gallus TNFRSF23 are
RT expressed in the ovary and differentially regulated by cell signaling
RT pathways.";
RL Biol. Reprod. 70:972-979(2004).
DR EMBL; AY251409; AAP41834.1; -.
DR HSSP; O14763; IDU3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4Fe4S FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS01186; EGF 2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 225 AA; 24697 MW; 59FC9C0AE4530630 CRC64;

Query Match 28.4%; Score 286.5; DB 2; Length 225;
Best Local Similarity 39.6%; Pred. No. 5e-17;
Matches 59; Conservative 26; Mismatches 53; Indels 11; Gaps 5;

Qy 19 RLLLLLLLLLPLQVFKFAMLELHSPK-PAGEYWSKDVCKKNCAGTFVKAPCEIPHT 78
Db 4 RAVGLLLLVLTITVP-----GSXAEV---CGEYLXEDICCMCLCPAGTYVAQHCRIPHS 55
Qy 79 QGQCEKCHPG-TFTEKDYLDACILCTCDKQEMVADCSATSDRKQCQRTGLYYDPKF 137
Db 56 RGKASCCTEGRDYTAHANGUECLLCRQCKDDQITLRTCTVTSDEQCQHG-YFCPAEG 114
Qy 138 PESCRPCTK-CPOGIPVLQECNSTANTVC 165
Db 115 CEICQRCCTCPEGREIVQICNATMDLGC 143

RESULT 5
Q7T3M8
ID Q7T3M8 PRELIMINARY; PRT; 410 AA.
AC Q7T3M8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

```

```

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Death domain-containing tumor necrosis factor receptor superfamily
DE member 23 variant 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP BRIDGHAM J.T., JOHNSON A.L.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251408; AAP41833.1; -.
DR HSSP; O14763; IDU3.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4Fe4S FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF 2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON TER 410 410
SQ SEQUENCE 410 AA; 46194 MW; 4BFCT7016C2BA60 CRC64;

Query Match 28.4%; Score 286.5; DB 2; Length 410;
Best Local Similarity 39.6%; Pred. No. 8.7e-17;
Matches 59; Conservative 26; Mismatches 53; Indels 11; Gaps 5;

Qy 19 RLLLLLLLLLPLQVFKFAMLELHSPK-PAGEYWSKDVCKKNCAGTFVKAPCEIPHT 78
Db 4 RAVGLLLLVLTITVP-----GSXAEV---CGEYLXEDICCMCLCPAGTYVAQHCRIPHS 55
Qy 79 QGQCEKCHPG-TFTEKDYLDACILCTCDKQEMVADCSATSDRKQCQRTGLYYDPKF 137
Db 56 RGKASCCTEGRDYTAHANGUECLLCRQCKDDQITLRTCTVTSDEQCQHG-YFCPAEG 114
Qy 138 PESCRPCTK-CPOGIPVLQECNSTANTVC 165
Db 115 CEICQRCCTCPEGREIVQICNATMDLGC 143

RESULT 6
Q9DFV0
ID Q9DFV0 PRELIMINARY; PRT; 438 AA.
AC Q9DFV0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ovarian TNF receptor.
GN Name=tnfrsf1a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Boe J., Goetz F.W.;
RT "Molecular cloning and expression of a TNF receptor and two TNF
RL ligands in the fish ovary.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
DR EMBL; AF250042; AAC24365.1; -.

```

```
DR HSP; Q92956; LUMA.  
DR ZFIN; ZDB-GENE-010802-1; tnfrsf1.  
DR GO; GO:0005515; P:protein binding; IEA.  
DR GO; GO:0004872; P:receptor activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000345; CytC_heme_BS.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH_like.  
DR InterPro; IPR001368; TNFR_C6.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00020; TNFR_C6; 2.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00150; CYTOCHROME_C; UNKNOWN_1.  
DR PROSITE; PS00017; DEATH_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR_NGFR_1; 1.  
DR PROSITE; PS00050; TNFR_NGFR_2; 2.  
KW Receptor.  
SQ SEQUENCE 438 AA; 49103 MW; B7E5312BE6B80B04 CRC64;  
  
Query Match 27.3%; Score 275.5; DB 2; Length 438;  
Best Local Similarity 39.2%; Pred. No. 8.3e-16;  
Matches 49; Conservative 18; Mismatches 51; Indels 7; Gaps 1;  
  
QY 41 LELHSFKCPAGEYMSKDVCKKNSAGTFVKAPCEIHTQGCCEKCHPGTFTEKDNVLDAC 100  
DB 45 LENH-----EYPHNGFCCKNCEAGTYVKEKCTSGHVMGKSPCKGTVAEHTGMEQC 97  
QY 101 ILCTGCDKQEMVADCSATSDRCQCRCTGLYYDPKPPESCRCPTCKPQGIPLVQECNST 160  
DB 98 LQSCQCHRDVTVAECTISTNTKCDCKFGTFCFLPDEPCEVCKCTCKADEEVSCTPT 157  
QY 161 ANTVK 165  
DB 158 SNTKC 162  
  
RESULT 7  
ID Q800K8 PRELIMINARY; PRT; 395 AA.  
AC Q800K8;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Tumor necrosis factor receptor-1.  
GN Name=TNFR-1;  
OS Paralicthys olivaceus (Japanese flounder).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Pleuronectoidei; Paralicthyidae; Paralicthys.  
OC NCBI_TaxID=8255;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22518447; PubMed=12631519; DOI=10.1016/S0145-305X(02)00118-0;  
RA Park C., Kurobe T., Hirano I., Aoki T.;  
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis  
factor receptor superfamily genes from Japanese flounder Paralicthys  
olivaceus".  
RL Dev. Comp. Immunol. 27:365-375 (2003).  
DR EMBL; AB080946; BAC65225.1; -.  
DR HSP; O14763; IDU3.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH_like.  
DR InterPro; IPR001368; TNFR_C6.  
DR InterPro; IPR001878; Znf_CCHC.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00020; TNFR_C6; 2.  
DR SMART; SM00208; TNFR; 3.  
DR SMART; SM00343; Znf_C2HC; 2.  
  
DR HSP; Q92956; LUMA.  
DR ZFIN; ZDB-GENE-010802-1; tnfrsf1.  
DR GO; GO:0005515; P:protein binding; IEA.  
DR GO; GO:0004872; P:receptor activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000345; CytC_heme_BS.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH_like.  
DR InterPro; IPR001368; TNFR_C6.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00020; TNFR_C6; 2.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00150; CYTOCHROME_C; UNKNOWN_1.  
DR PROSITE; PS00017; DEATH_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR_NGFR_1; 1.  
DR PROSITE; PS00050; TNFR_NGFR_2; 2.  
KW Receptor.  
SQ SEQUENCE 438 AA; 49103 MW; B7E5312BE6B80B04 CRC64;  
  
Query Match 27.3%; Score 275.5; DB 2; Length 438;  
Best Local Similarity 39.2%; Pred. No. 8.3e-16;  
Matches 49; Conservative 18; Mismatches 51; Indels 7; Gaps 1;  
  
QY 41 LELHSFKCPAGEYMSKDVCKKNSAGTFVKAPCEIHTQGCCEKCHPGTFTEKDNVLDAC 100  
DB 45 LENH-----EYPHNGFCCKNCEAGTYVKEKCTSGHVMGKSPCKGTVAEHTGMEQC 97  
QY 101 ILCTGCDKQEMVADCSATSDRCQCRCTGLYYDPKPPESCRCPTCKPQGIPLVQECNST 160  
DB 98 LQSCQCHRDVTVAECTISTNTKCDCKFGTFCFLPDEPCEVCKCTCKADEEVSCTPT 157  
QY 161 ANTVK 165  
DB 158 SNTKC 162  
  
RESULT 7  
ID Q800K8 PRELIMINARY; PRT; 395 AA.  
AC Q800K8;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Tumor necrosis factor receptor-1.  
GN Name=TNFR-1;  
OS Paralicthys olivaceus (Japanese flounder).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Pleuronectoidei; Paralicthyidae; Paralicthys.  
OC NCBI_TaxID=8255;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22518447; PubMed=12631519; DOI=10.1016/S0145-305X(02)00118-0;  
RA Park C., Kurobe T., Hirano I., Aoki T.;  
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis  
factor receptor superfamily genes from Japanese flounder Paralicthys  
olivaceus".  
RL Dev. Comp. Immunol. 27:365-375 (2003).  
DR EMBL; AB080946; BAC65225.1; -.  
DR HSP; O14763; IDU3.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH_like.  
DR InterPro; IPR001368; TNFR_C6.  
DR InterPro; IPR001878; Znf_CCHC.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00020; TNFR_C6; 2.  
DR SMART; SM00208; TNFR; 3.  
DR SMART; SM00343; Znf_C2HC; 2.  
  
DR PROSITE; PS00017; DEATH_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.  
DR PROSITE; PS00050; TNFR_NGFR_2; 2.  
KW Receptor.  
SQ SEQUENCE 395 AA; 44304 MW; 8D685A9F74710AE1 CRC64;  
  
Query Match 27.1%; Score 273.5; DB 2; Length 395;  
Best Local Similarity 34.1%; Pred. No. 1.1e-15;  
Matches 58; Conservative 28; Mismatches 75; Indels 9; Gaps 2;  
  
QY 20 RLILLILLILLNLP-LQVKFAMLELHSHFKCPAGEYMSKDVCKKNSAGTFVKAPCEIHT 78  
DB 9 RLIVLLSSGTGVPQSRIDFGRRTORCILCSNDQNLGNCCNCPAGTHVSHCSKSGE 68  
QY 79 QGQCEKCHPGTFTEKDNVLDACILCTGCDKQEMVADCSATSDRCQCRCTGLYYDPKFP 138  
DB 69 KGQCECDYRTVTAHPNELNQCFPCRPDPDQIVTFCLTTQDTECCAKAGFCDFPHQAC 128  
QY 139 ESCRCPTCKPQGIPLVQECNSTANTVC-----SSSVSRSSASVAWPI 180  
DB 129 EVCKCKCKCKDEIBEIRNCTSTTTECKIKPNKSGSAGNKQVIAVVFPI 178  
  
RESULT 8  
ID Q9DF34 PRELIMINARY; PRT; 357 AA.  
AC Q9DF34;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Death receptor.  
GN Name=hdr;  
OS Brachydanio rerio (zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OC NCBI_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20394298; PubMed=10934476; DOI=10.1038/35019592;  
RA Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;  
RT "Stimulation of erythropoiesis by inhibiting a new hematopoietic death  
receptor in transgenic zebrafish".  
RL Nat. Cell Biol. 2:549-552 (2000).  
DR EMBL; AF302789; AAG21396.1; -.  
DR HSP; Q92956; LUMA.  
DR ZFIN; ZDB-GENE-030826-5; hdr.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH_like.  
DR InterPro; IPR001368; TNFR_C6.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00020; TNFR_C6; 3.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00017; DEATH_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR_NGFR_1; 3.  
DR PROSITE; PS00050; TNFR_NGFR_2; 2.  
KW Receptor.  
SQ SEQUENCE 357 AA; 40662 MW; 1652B4840D9EDBA CRC64;  
  
Query Match 25.7%; Score 259; DB 2; Length 357;  
Best Local Similarity 32.9%; Pred. No. 1.8e-14;  
Matches 56; Conservative 28; Mismatches 70; Indels 16; Gaps 3;  
  
QY 20 RLILLILLILLNLP-LQVKFAMLELHSHFKCPAG-FYWSKDVCKKNSA 65  
DB 2 RYITLLVLLLVNINAAARSHGDLAWAHSVKNRL--SRDVSREGLEYPHENICCLNCPA 59  
QY 66 GTFVKAPCEIHTQGCCEKCHPGTFTEKDNVLDACILCTGCDKQEMVADCSATSDRCQ 125  
DB 60 GTYVKKACAAAABKGVCAPCFDTTTEHDHGLLKICISCDKCRIDQETIEKTSTQNTCK 119
```

Qy 126 CRTGLYYDPKPPESCRPTCKPQGIPLVQCNCSTANTVCSSSVRRSAS 175
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 120 CRNGSFCLPDCAECVKIGSRCKEDETEKSCTAISNTVCRKNSPGS 169

RESULT 9

ID	Q6D081	PRELIMINARY;	PRT;	321 AA.
AC	Q6D081;			
DC	25-OCT-2004	(TREMBLrel. 28, Created)		
DT	25-OCT-2004	(TREMBLrel. 28, Last sequence update)		
DT	25-OCT-2004	(TREMBLrel. 28, Last annotation update)		
DE	MGC88957 protein.			
GN	Name=MGC88957;			
OS	Xenopus tropicalis (Western clawed frog) (<i>Silurana tropicalis</i>).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8364;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Whole body;			
RX	MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.S			
RA	Villalón D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S			
RA	Richardson D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield			
RA	Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad.Sci. U.S.A. 99:16899-16903(2002).			

RP SEQUENCE FROM N.A.
RC TISSUE=whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the ENBL/GenBank/DDSV databases.

GO:	GO:0005515:	F-protein binding; IEA.	
DR	GO:	GO:0004872:	P-receptor activity; IEA.
DR	GO:	GO:0071651:	P-signal transduction; IEA.
DR	InterPro:	IPR0001450:	4Fe4S ferredoxin; IEA.
DR	InterPro:	IPR000345:	CytC heme_BS.
DR	InterPro:	IPR000488:	Death.
DR	InterPro:	IPR011029:	DEATH like.
DR	InterPro:	IPR001368:	TNFR_c6

DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.

DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 1.

SQ SEQUENCE 321 AA; 36225 MW; 21E69219ABB34673 CRC64;

Query Match	24.8%	Score 249.5;	DB 2;	Length 321;
Best Local Similarity	33.3%	Pred. No. 1.1e-13;		
Matches	59;	Conservative	23;	Mismatches 64;
				Indels 31

Qy	63	4	FC	SLVSSLSRWFLWRRLLLLLLLLLLNLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNC	63
Db		8	FC	-----IFLLAAPTITGLPLPUS-----SDLY-----YQENIRCLRC	40
Qy	1222	64	SAGT	TVKAPCELPHTQGOCEKHG-PTEKDNVLDACILCSTCKDQDWADCSATSDR	1222
Db		41	PAGT	TVKPCPTKPTDIGSCSCHTGSTYSEGPTGLDHCLTCLRCDDQEVREPTCTAQA	100
Qy	178	123	KQCR	TGLYYDDPKPEPSCRCT-KCQGIPLVQECNSTANTVCCSSSVSRSSASVAM	178
Db		101	ECRC	KKGYCPIDHPCEVCLCTBEKCPGGBLOPCCNSTSDSCGPAES-GSWIWM	155

RESIST 10

Q70593	Q76B99	PRELIMINARY;	PRT;	328 AA.
AC	Q76B99;			
AD	05-JUL-2004	(TrEMBLrel. 27, Created)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	Death receptor-M1.			
DE	Name=xDR-M1;			
GN	Xenopus laevis (African clawed frog).			
OS	Xenopus laevis; Chordata: Craniata: Vertebrata; Euteleostomi;			
OC	Eukaryota; Metazoa; Chordata: Craniata: Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
ON	NCBI_TaxID=8355;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RP	PubMed=14668340; DOI=10.1074/jbc.M306217200;			
RA	Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;			
RA	"Xenopus death receptor-M1 and -M2, new members of the tumor necrosis			
RT	factor receptor superfamily, trigger apoptotic signaling by			
RT	differential mechanisms".			
RL	J. Biol. Chem. 279:7629-7635(2004).			
DR	ENBL; AB11446; BAD11770.1; -.			
DR	GO; GO:0005515; F:protein binding; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0007165; P:signal transduction; IEA.			
DR	InterPro; IPR001450; 4Fe4S_ferredoxin.			
DR	InterPro; IPR000488; Death.			
DR	InterPro; IPR011029; DEATH_like.			
DR	InterPro; IPR001368; TNFR_c6.			
DR	Pfam; PF00531; Death; 1.			
DR	Pfam; PF00020; TNFR_c6; 1.			
DR	SMART; SM00005; DEATH; 1.			
DR	SMART; SM00208; TNFR; 3.			
DR	DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.			
DR	DR PROSITE; PS00117; DEATH_DOMAIN; 1.			
DR	DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.			
DR	DR PROSITE; PS00500; TNFR_NGFR_2; 2.			
DR	Receptor.			
QX	SEQUENCE	328 AA;	37252 MW;	444D62A8ACBF9525 CRC64;

Query Match 24.7%; Score 249; DB 2; Length 328;
Best Local Similarity 38.3%; Pred. No. 1.2e-13;
Matches 49; Conservative 22; Mismatches 55; Indels

[illegible]

RESULT 11
Q6GLZ4


```
RA Duthie S., Nasir L., Eckersall P.D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.
DR HSSP; P19438; 1EXT.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR008209; EGF_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON TER 189
SQ SEQUENCE 189 AA; 21420 MW; F3FB50CB809D7DBE CRC64;

Query Match 23.7%; Score 239; DB 2; Length 189;
Best Local Similarity 35.3%; Pred. No. 5.5e-13;
Matches 55; Conservative 19; Mismatches 70; Indels 12; Gaps 5;

Qy 22 LLLLLLLLLLPLOVKFAM-----LELHSPKCPAGEY---WSKDVCCCKNSAGTFVKAPC 73
Db 13 LVLLALLVEIYPLRVTLGLVPHLRDREKRAIPCPQGGYIHPQDINSICCTCKHKGTYLYNDC 72
Qy 74 EIPHTQGCCKCHPGTFTKDNVLDACILGSTCDKD--QEMVADCSATSDRKQCCRTGLY 131
Db 73 EGPGLDTRDCECENGTTFTASENYLRQCLSCSKCKEMYQVEISPTVYRDTVCGCRNQY 132
Qy 132 -YDPKFPESCRCPTKCPQIGIPVLQECNSTANTVCS 166
Db 133 RYWSETHFOCLNCSLCLNG-TVQISCKETQNTVCT 167

RESULT 14
Q95ND3 PRELIMINARY; PRT; 446 AA.
AC Q95ND3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor necrosis factor type I.
GN Name=TNFR I;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21425403; PubMed=11531421; DOI=10.1006/viro.2001.1042;
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT "TNF-alpha-induced cell death in feline immunodeficiency virus-
infected cells is mediated by the caspase cascade.";
RL Virology 287:446-455(2001).
DR EMBL; AB051103; BAB55455.1; -.
DR HSSP; P19438; 1ICH.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.

Qy 22 LLLLLLLLLLPLOVKFAM-----LELHSPKCPAGEY---WSKDVCCCKNSAGTFVKAPC 73
Db 13 LVLLALLVEIYPLRVTLGLVPHLRDREKRAIPCPQGGYIHPQDINSICCTCKHKGTYLYNDC 72
Qy 74 EIPHTQGCCKCHPGTFTKDNVLDACILGSTCDKD--QEMVADCSATSDRKQCCRTGLY 131
Db 73 EGPGLDTRDCECENGTTFTASENYLRQCLSCSKCKEMYQVEISPTVYRDTVCGCRNQY 132
Qy 132 -YDPKFPESCRCPTKCPQIGIPVLQECNSTANTVCS 166
Db 133 RYWSETHFOCLNCSLCLNG-TVQISCKETQNTVCT 167

RESULT 15
Q76B98 PRELIMINARY; PRT; 328 AA.
AC Q76B98;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Death receptor-M2.
GN Name=xDR-M2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14668340; DOI=10.1074/jbc.M306217200;
RA Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;
RT "Xenopus death receptor-M1 and -M2, new members of the tumor necrosis
factor receptor superfamily, trigger apoptotic signaling by
differential mechanisms.";
RL J. Biol. Chem. 279:7629-7635(2004).
DR EMBL; AB11447; BAD1171.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Pe4s_ferredoxin.
DR InterPro; IPR000488; Death_like.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4PE4S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 328 AA; 36586 MW; 3FCD1CCAB8533355 CRC64;

Query Match 23.0%; Score 232; DB 2; Length 328;
Best Local Similarity 32.7%; Pred. No. 3.7e-12;
Matches 56; Conservative 22; Mismatches 63; Indels 30; Gaps 4;

Qy 2 FGFFCSLVSSLSRFLWRLRLLLLLLLLLLNLPLQVKFAMLELHSPKCPAGEYWSKDVCCCK 61
Db 18 FGFFS-----FLIVSTNGLPLP-----PENYYQAGNTRCL 49
Qy 62 NCSAGTFVKAPCBIPHTQGCCKCHPG-TFTEKDNVLDACILGSTCDKDQEMVADCSATS 120
Db 50 RCPAGTYVGMPCFTTQDTVGKCFPCHTGSSPSEGFTGLDHCLTCLSCRDDQEEVRPCTATQ 109
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 17:05:32 ; Search time 544.286 Seconds
(without alignments)
127.905 Million cell updates/sec

Title: US-10-622-407-10

Perfect score: 1008

Sequence: 1 MFGFFCSLVSLSRFLWRR.....ANTVCSVVSRBSASVAVPI 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008	100.0	180	7	ABW02716
2	1008	100.0	180	8	ADJ45754
3	956	94.8	198	7	ABW02715
4	956	94.8	198	8	ADJ45752
5	956	94.8	398	7	ABW02717
6	956	94.8	398	8	ADJ45758
7	748	74.2	133	7	ABW02714
8	748	74.2	133	8	ADJ45750
9	709	70.3	396	8	ADF57557
10	705	69.9	176	2	AAW80254
11	705	69.9	176	8	ADF57551
12	705	69.9	176	8	ADMA46623
13	641	63.6	148	8	ADMA46624
14	542.5	53.8	380	4	ABG09344
15	467	46.3	117	8	ADF57549
16	299	29.7	204	5	ABBB1467
17	217.5	21.6	247	8	ADF57553
18	217.5	21.6	454	5	AAO22289
19	217.5	21.6	454	8	ADT08167
20	208.5	20.7	355	2	AAR85073
21	208.5	20.7	355	4	AAAB50524
22	208.5	20.7	355	8	ADJ96165
23	207.5	20.6	285	2	AAW33359
24	205	20.3	350	5	ABBB1468
25	204.5	20.3	461	7	ADE57927

26	204.5	20.3	461	8	ADQ76809
27	203.5	20.2	256	2	AAW33357
28	203.5	20.2	307	2	AAW33358
29	203.5	20.2	336	2	AAW33360
30	203.5	20.2	461	2	ABG74754
31	203.5	20.2	461	2	AAR07450
32	203.5	20.2	884	2	AAR70109
33	202.5	20.1	658	5	AAW49759
34	201.5	20.0	168	2	AAR24084
35	201.5	20.0	197	6	ADA49707
36	201.5	20.0	199	2	AAR24080
37	201.5	20.0	211	2	AAW89225
38	201.5	20.0	213	6	ABB95540
39	201.5	20.0	219	8	ADR90159
40	201.5	20.0	240	8	ADR90162
41	201.5	20.0	247	6	ADA09864
42	201.5	20.0	270	8	ADR90160
43	201.5	20.0	280	4	AAW66979
44	201.5	20.0	280	8	ADM28817
45	201.5	20.0	306	8	ADR90161

Adq76809 Rat solub
Aaw33357 TBP(20-16
Aaw33358 TBP(20-16
Aaw33360 TBP(20-19
Abg74754 Rat TNF-R
Aar07450 Rat Tumou
Aar70109 TNF-R-GBP
Aam49759 TNF-selec
Aar24084 Truncated
Ada49707 Extracell
Aar24080 Truncated
Aaw89225 Tumour ne
Abb95540 Amino aci
Adr90159 Human tum
Adr90162 Human tum
Ada09864 Human rec
Adr90160 Human tum
Aab66979 Tnfr1 pro
Adm28817 TNFR supe
Adr90161 Human tum

ALIGNMENTS

RESULT 1

ABW02716

ID ABW02716 standard; protein; 180 AA.

XX AC ABW02716;

XX DT 11-MAR-2004 (first entry)

XX DE Mouse tmst2-receptor splice variant protein.

XX KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;

XX KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;

XX KW cancer; chromosome identification; gene therapy; antibacterial; virucide;

XX KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;

XX KW cytostatic; mouse; splice variant.

XX OS Mus musculus.

XX PN US6627199-B1.

XX PD 30-SEP-2003.

XX PF 07-JUL-2000; 2000US-00612033.

XX PR 09-JUL-1999; 99US-0143063P.

XX PA (AMGE-) AMGEN INC.

XX PI Saris C;

XX DR WPI; 2003-874309/81.

XX DR N-PSDB; AAD64755.

XX PT New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,

XX PT treating or ameliorating diseases associated with or resulting from

XX PT abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for

XX PT chromosome mapping.

XX PS Claim 1; SEQ ID NO 10; Opp; English.

XX CC The invention relates to transmembrane decoy-receptor (tmst2) proteins

XX CC and their secreted splice variants, belonging to the tumour necrosis

XX CC factor (TNF) receptor super gene family and polynucleotides encoding such

XX CC proteins. The composition and methods are useful in diagnosing, treating

XX CC or ameliorating diseases associated with or resulting from abnormal tmst2

XX CC and/or abnormal expression of its putative ligand, such as sepsis,

XX CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial

XX CC and parasitic diseases or cancer. They may also be used for chromosome

CC identification or mapping. The invention is useful in gene therapy. The
CC present sequence is mouse tmst2-receptor splice variant protein used in
CC the exemplification of the invention

Sequence 180 AA:

	Query Match	100.0%;	Score 1008;	DB 7;	Length 180;
	Best Local Similarity	100.0%;	Prod. No. 2e-75;		
	Matches 180;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGFFCSSLVSSGRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLELHSPKCPAGEYMSKDVC	60		
Db	1	MGFFCSSLVSSGRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLELHSPKCPAGEYMSKDVC	60		
Qy	61	KNCAGTFVKAPEIPIHTQGCQEKCHPGTTEKQNYLDACILCSTCKDQEWADCSATS	120		
Db	61	KNCAGTFVKAPEIPIHTQGCQEKCHPGTTEKQNYLDACILCSTCKDQEWADCSATS	120		
Qy	121	DRKQCRTGLIYYDPEKPEPCRPCTKCPQIGIVLQECNSTANTVCCSSSVRRSASVAWPI	180		
Db	121	DRKQCRTGLIYYDPEKPEPCRPCTKCPQIGIVLQECNSTANTVCCSSSVRRSASVAWPI	180		

RESULT 2

ADJ45754
ID ADJ45754 standard; protein; 180 AA.

AA
AC
ADJ45754;

06-MAY-2004 (first entry)

DE Murine tmst2-receptor splice variant polypeptide.

Mouse; tm2s2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria; diabetes mellitus; disseminated intravascular coagulation; haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia; lymphoma; meningitis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease; tm2s2-receptor splice variant; receptor.

XX
OS
Mus musculus.

XX PN US2004018544-A1.

XX
PD 29-JAN-2004.XX
PF 17-JUL-2003: 2003US-00622407.XX
PR 09-JUL-1999 99US-0143063P

PR 07-JUL-2000; 2000US-00612033.
XX

PA (SARI//) SARIS C.
XY

PI Saris C;
yy

DR WPI; 2004-224390/21.
DR N-DEPB. 201457E2.

XX
DT
Nov 17 1964

PT disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial infections

XX
pg
XX
Classification 12. SEC TO NO 10. 5700. English

xx The invention relates to a tm22-receptor polypeptides and the
 CC polynucleotide encoding them. The sequences of the invention are useful
 CC for treating diseases and conditions including acquired immunodeficiency
 CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral
 CC malaria, diabetes mellitus, disseminated intravascular coagulation,
 CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,
 CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ

CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory
CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.
CC This sequence represents a murine tmst2-receptor splice variant
CC polypeptide of the invention.

XX
SO
Sequence 180 AA:

Query Match	100.0%;	Score 1008;	DB 8;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 2e-75;		
Matches 180;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

RESULT 3

ABW02715
ID ABW02715 standard; protein; 198 AA.

AC ABW02715;

11-MAR-2004 (first entry)

XX
DE
Mouse tmst2-receptor protein.

Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
cachexia; autoimmune disease; inflammatory disease; chromosome mapping;
cancer; chromosome identification; gene therapy; antibacterial; virucide;
immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
cystostatic; mouse.

XX
QS
MiscellaneousXX
PN
US6627199-B1XX
PD
30-SEP-2003.XX
PF 07-JUL-2000: 2000US-00612033.XX
PR 09-JUL-1999: 99US-0143063P.

PA (AMGE-) AMGEN INC.

XX
PT
Sarg C:XX
DB WPT: 2003-874309/81

DR N-PSDB; AAD64/54.
YY

PT New *ttnst2* nucleic acid molecule and polypeptide, useful for diagnosing
PT treating or ameliorating diseases associated with or resulting from
PT abnormal *ttnst2* expression, e.g. sepsis, inflammation or cancer, or for
PT chromosome mapping.

XX
PS
Claim 1: SEQ ID NO 8: Opp: English.

XX The invention relates to transmembrane decoy-receptor (tmst2) proteins
CC and their secreted splice variants, belonging to the tumour necrosis
CC factor (TNF) receptor super gene family and polynucleotides encoding such
CC proteins. The composition and methods are useful in diagnosing, treating
CC or ameliorating diseases associated with or resulting from abnormal tmst2
CC and/or abnormal expression of its putative ligand, such as sepsis,
CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial
CC and parasitic diseases or cancer. They may also be used for chromosome
CC identification or mapping. The invention is useful in gene therapy. The

```
CC present sequence is mouse tmst2-receptor protein used in the
CC exemplification of the invention
XX
SQ Sequence 198 AA;

Query Match          94.8%; Score 956; DB 7; Length 198;
Best Local Similarity 100.0%; Pred. No. 4.4e-71;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFFCSLVSSLSRWFLWRRLRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
DB 1 MFGFFCSLVSSLSRWFLWRRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
QY 61 KNCAGTFVKAPEIPTHQGCCKCHPGTTEKDNVLDACILCSTCDKQEWVADCSATS 120
DB 61 KNCAGTFVKAPEIPTHQGCCKCHPGTTEKDNVLDACILCSTCDKQEWVADCSATS 120
QY 121 DRKCQCRGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170
DB 121 DRKCQCRGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170

RESULT 4
ADJ45752
ID ADJ45752 standard; protein; 198 AA.
XX
AC ADJ45752;
DT 06-MAY-2004 (first entry)
XX
DE Murine tmst2-receptor.
XX
KW Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;
KW autoimmune disease; cachexia; cancer; cerebral malaria;
KW diabetes mellitus; disseminated intravascular coagulation;
KW haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;
KW lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;
KW organ rejection; rheumatoid arthritis; septic shock; stroke;
KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
KW receptor.
XX
OS Mus musculus.
XX
PN US2004018544-A1.
XX
PD 29-JAN-2004.
XX
PF 17-JUL-2003; 2003US-00622407.
XX
PR 09-JUL-1999; 99US-0143063P.
XX
PR 07-JUL-2000; 2000US-00612033.
XX
PA (SARI/) SARIS C.
XX
PI Saris C;
XX
WPI; 2004-224390/21.
XX
N-PSDB; ADJ45751.
XX
Novel tmst2-receptor polypeptide useful for diagnosing and treating
disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
infections.
XX
Claim 13; SEQ ID NO 8; 57pp; English.
XX
The invention relates to a tmst2-receptor polypeptides and the
polynucleotide encoding them. The sequences of the invention are useful
for treating diseases and conditions including acquired immunodeficiency
syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral
malaria, diabetes mellitus, disseminated intravascular coagulation,
haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,
lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ
rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory
```

```
CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.
CC This sequence represents the murine tmst2-receptor polypeptide of the
CC invention.
XX
SQ Sequence 198 AA;

Query Match          94.8%; Score 956; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. No. 4.4e-71;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFFCSLVSSLSRWFLWRRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
DB 1 MFGFFCSLVSSLSRWFLWRRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
QY 61 KNCAGTFVKAPEIPTHQGCCKCHPGTTEKDNVLDACILCSTCDKQEWVADCSATS 120
DB 61 KNCAGTFVKAPEIPTHQGCCKCHPGTTEKDNVLDACILCSTCDKQEWVADCSATS 120
QY 121 DRKCQCRGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170
DB 121 DRKCQCRGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170

RESULT 5
ABW02717
ID ABW02717 standard; protein; 398 AA.
XX
AC ABW02717;
DT 11-MAR-2004 (first entry)
XX
DE Mouse tmst2-receptor-human immunoglobulin Fc region fusion protein.
XX
KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;
KW cancer; chromosome identification; gene therapy; antibacterial; virucide;
KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
KW cytostatic; mouse; human; immunoglobulin Fc region; fusion protein.
XX
OS Chimeric - Mus musculus.
XX
OS Chimeric - Homo sapiens.
XX
PN US6627199-B1.
XX
PD 30-SEP-2003.
XX
PF 07-JUL-2000; 2000US-00612033.
XX
PR 09-JUL-1999; 99US-0143063P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Saris C;
XX
WPI; 2003-874309/81.
XX
N-PSDB; AAD64758.
XX
New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,
treating or ameliorating diseases associated with or resulting from
abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
chromosome mapping.
XX
Example 4; SEQ ID NO 14; 0pp; English.
XX
The invention relates to transmembrane decoy-receptor (tmst2) proteins
and their secreted splice variants, belonging to the tumour necrosis
factor (TNF) receptor super gene family and polynucleotides encoding such
proteins. The composition and methods are useful in diagnosing, treating
or ameliorating diseases associated with or resulting from abnormal tmst2
or/and/or abnormal expression of its putative ligand, such as sepsis,
cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial
and parasitic diseases or cancer. They may also be used for chromosome
identification or mapping. The invention is useful in gene therapy. The
```

CC present sequence is a fusion protein comprising mouse tmst2- receptor
 CC protein and human immunoglobulin Fc region. This sequence is used in the
 CC exemplification of the invention
 XX
 SQ Sequence 398 AA;

Query Match 94.8%; Score 956; DB 7; Length 398;
 Best Local Similarity 100.0%; Pred. No. 8.8e-71;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
 Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCEKCHPGTFTEKDNLYDACILCSTCDKQEMVADCSATS 120
 Db 61 KNCAGTFVKAPCEIPHTQGCCEKCHPGTFTEKDNLYDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSVS 170
 Db 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSVS 170

RESULT 6
 ADJ45758
 ID ADJ45758 standard; protein; 398 AA.
 AC ADJ45758;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Murine tmst2-Fc fusion protein.
 XX
 KW Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;
 KW autoimmune disease; cachexia; cancer; cerebral malaria;
 KW diabetes mellitus; disseminated intravascular coagulation;
 KW haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;
 KW lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;
 KW organ rejection; rheumatoid arthritis; septic shock; stroke;
 KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
 KW tmst2-Fc fusion protein; receptor.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 XX US2004018544-A1.
 XX
 XX 29-JAN-2004.
 XX
 XX 17-JUL-2003; 2003US-00622407.
 XX
 XX 09-JUL-1999; 99US-0143063P.
 XX 07-JUL-2000; 2000US-00612033.
 XX
 XX (SARI/) SARIS C.
 XX
 XX Saris C;
 XX
 XX WPI; 2004-224390/21.
 XX N-PSDB; ADJ45757.
 XX
 XX Novel tmst2-receptor polypeptide useful for diagnosing and treating
 XX disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
 XX infections.
 XX
 XX Example 4; SEQ ID NO 14; 57pp; English.
 XX
 XX The invention relates to a tmst2-receptor polypeptides and the
 XX polynucleotide encoding them. The sequences of the invention are useful
 XX for treating diseases and conditions including acquired immunodeficiency
 XX syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral
 XX malaria, diabetes mellitus, disseminated intravascular coagulation,
 XX haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,

CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ
 CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory
 CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.
 CC This sequence represents a murine tmst2-Fc fusion protein of the
 CC invention.
 XX
 SQ Sequence 398 AA;

Query Match 94.8%; Score 956; DB 8; Length 398;
 Best Local Similarity 100.0%; Pred. No. 8.8e-71;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
 Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCEKCHPGTFTEKDNLYDACILCSTCDKQEMVADCSATS 120
 Db 61 KNCAGTFVKAPCEIPHTQGCCEKCHPGTFTEKDNLYDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSVS 170
 Db 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSVS 170

RESULT 7
 ABW02714
 ID ABW02714 standard; protein; 133 AA.
 AC ABW02714;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Mouse tmst2-receptor protein from tmst2-00004-d1 clone.
 XX
 KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
 KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;
 KW cancer; chromosome identification; gene therapy; antibacterial; virucide;
 KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
 KW cytotstatic; mouse.
 XX
 OS Mus musculus.
 XX
 XX US6627199-B1.
 XX
 XX 30-SEP-2003.
 XX
 XX 07-JUL-2000; 2000US-00612033.
 XX
 XX 09-JUL-1999; 99US-0143063P.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Saris C;
 XX
 XX WPI; 2003-874309/81.
 XX N-PSDB; AAD64753.
 XX
 XX New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,
 XX treating or ameliorating diseases associated with or resulting from
 XX abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
 XX chromosome mapping.
 XX
 XX Example 1; SEQ ID NO 6; Opp; English.
 XX
 XX The invention relates to transmembrane decoy-receptor (tmst2) proteins
 XX and their secreted splice variants, belonging to the tumour necrosis
 XX factor (TNF) receptor super gene family and polynucleotides encoding such
 XX proteins. The composition and methods are useful in diagnosing, treating
 XX or ameliorating diseases associated with or resulting from abnormal tmst2
 XX and/or abnormal expression of its putative ligand, such as sepsis,
 XX cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial
 XX and parasitic diseases or cancer. They may also be used for chromosome

CC identification or mapping. The invention is useful in gene therapy. The
 CC present sequence is mouse tmst2-receptor protein used in the
 CC exemplification of the invention
 XX
 SQ Sequence 133 AA;

Query Match 74.2%; Score 748; DB 7; Length 133;
 Best Local Similarity 100.0%; Pred. No. 4.4e-54;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
 Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
 Qy 61 KNCAGTFVVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQDQEMVADCSATS 120
 Db 61 KNCAGTFVVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQDQEMVADCSATS 120
 Qy 121 DRKQCRTGLYYY 133
 Db 121 DRKQCRTGLYYY 133

RESULT 8
 ADJ45750
 ID ADJ45750 standard; protein; 133 AA.
 AC ADJ45750;
 DT 06-MAY-2004 (first entry)
 XX
 DE Murine tmst2 00004-d1 polypeptide.
 XX
 KW Mouse; tmst2-receptor; tmst2 00004-d1;
 KW acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease;
 KW cachexia; cancer; cerebral malaria; diabetes mellitus; shock; hepatitis;
 KW disseminated intravascular coagulation; haemorrhagic shock; hepatitis;
 KW insulin resistance; leprosy; leukaemia; lymphoma; meningitis;
 KW multiple sclerosis; ischaemia; obesity; organ rejection;
 KW rheumatoid arthritis; septic shock; stroke;
 KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
 KW receptor.
 XX
 OS Mus musculus.
 XX
 PN US2004018544-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 17-JUL-2003; 2003US-00622407.
 XX
 PR 09-JUL-1999; 99US-0143063P.
 PR 07-JUL-2000; 2000US-00612033.
 XX
 PA (SARI/) SARIS C.
 XX
 PI Saris C;
 XX
 DR WPI; 2004-224390/21.
 DR N-PSDB; ADJ45749.
 XX
 PT Novel tmst2-receptor polypeptide useful for diagnosing and treating
 PT disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
 PT infections.
 XX
 PS Example 1; SEQ ID NO 6; 57pp; English.
 XX
 CC The invention relates to a tmst2-receptor polypeptides and the
 CC polynucleotide encoding them. The sequences of the invention are useful
 CC for treating diseases and conditions including acquired immunodeficiency
 CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral
 CC malaria, diabetes mellitus, disseminated intravascular coagulation,
 CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,

CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ
 CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory
 CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.
 CC This sequence represents a murine tmst2-receptor polypeptide clone of the
 CC invention.
 XX
 SQ Sequence 133 AA;

Query Match 74.2%; Score 748; DB 8; Length 133;
 Best Local Similarity 100.0%; Pred. No. 4.4e-54;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
 Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
 Qy 61 KNCAGTFVVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQDQEMVADCSATS 120
 Db 61 KNCAGTFVVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQDQEMVADCSATS 120
 Qy 121 DRKQCRTGLYYY 133
 Db 121 DRKQCRTGLYYY 133

RESULT 9
 ADF57557
 ID ADF57557 standard; protein; 396 AA.
 XX
 AC ADF57557;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Mouse ymkz5-human Fc fusion protein.
 XX
 KW Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour;
 KW cancer; acquired immune deficiency syndrome; AIDS; anaemia;
 KW autoimmune disease; cachexia; leprosy; leukaemia; hepatitis;
 KW multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
 KW receptor; human.
 XX
 OS Chimeric.
 OS Mus musculus.
 OS Homo sapiens.
 XX
 PN US2003096355-A1.
 XX
 PD 22-MAY-2003.
 XX
 PF 11-JUL-2002; 2002US-00193616.
 XX
 PR 09-JUL-1999; 99US-0143137P.
 PR 07-JUL-2000; 2000US-00611989.
 XX
 PA (ZHAN/) ZHANG K.
 XX
 PI Zhang K;
 XX
 DR WPI; 2004-008943/01.
 XX
 PT Novel ymkz5-receptor polypeptide useful for treating diseases such as
 PT tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy,
 PT leukemia, hepatitis, multiple sclerosis.
 XX
 PS Example 4; SEQ ID NO 14; 57pp; English.
 XX
 CC The invention relates to transmembrane decoy receptor, ymkz5 belonging to
 CC tumour necrosis factor (TNF) receptor supergene family and nucleic acid
 CC sequences encoding such receptors. The invention is useful for detecting
 CC diseases or susceptibility to diseases related to the presence of mutated
 CC ymkz5-receptor gene such as tumours or cancers. The sequences of the
 CC invention are used as medication for a number of diseases such as
 CC acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases,

CC cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial
CC ischaemia, obesity etc. The invention is also useful in gene therapy. The
CC present sequence is mouse ymkz5-human Fc fusion protein.

SQ Sequence 396 AA;

Query Match 70.3%; Score 709; DB 8; Length 396;

Best Local Similarity 78.6%; Pred. No. 2.2e-50;
Matches 132; Conservative 6; Mismatches 22; Indels 8; Gaps 1;

QY 7 SLVSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCAG 66

Db 5 SHVSSLSHWF-----LLLLLLLLLPLVIFAMPESYSFNCPDGEYQSDNDVCKTCPSG 56

QY 67 TFVKAPCEIPHTQGCCKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATSDRKQC 126

Db 57 TFVKAPCKIPHTQGCCKCHPGTFTKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPESCRCCTKCPQIPVLQECNSTANTVCSSVSRRSA 174

Db 117 QIGLYYYDDPKFPESCRCCTKCPQIPVLQECNSTANTVCSSVSNAAA 164

RESULT 10

AAW80254
ID AAW80254 standard; protein; 176 AA.

XX AC AAW80254;

XX DT 28-JAN-1999 (first entry)

XX DE Amino acid sequence of protein 7F4.

XX KW Protein 7F4; differentiation; osteoblast cell; bone growth; bone sarcoma.

XX OS Unidentified.

FH Key Location/Qualifiers

FT Peptide 1..28

FT Protein /note= "signal peptide"

FT Protein 29..176

FT Protein /note= "mature protein"

XX WO9843998-A1.

XX PD 08-OCT-1998.

XX PF 01-APR-1998; 98WO-JP001511.

XX PR 01-APR-1997; 97JP-00099653.

XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX PI Kimura N, Toyoshima T;

XX WPI; 1998-568275/48.

XX DR N-PSDB; AAV68046.

XX Receptor protein inducing differentiation in osteoblast cells - has

XX extracellular region only and can be used for screening substances for

XX treatment of bone growth disorders.

XX Claim 1; Page 29-31; 51pp; Japanese.

XX The present sequence represents a protein designated 7F4. This protein is

XX capable of inducing differentiation in osteoblast cells. The protein may

XX be used to screen compounds for the ability to bind to it, for use as

XX ligands, agonists or antagonists and inhibiting or otherwise altering its

XX differentiation inducing activity. Compounds so identified, as well as

XX the protein itself, DNA encoding it, and antibodies to it, may be used in

XX the treatment of diseases of bone growth and osteoblast differentiation,

XX such as bone sarcomas

SQ Sequence 176 AA;

Query Match 69.9%; Score 705; DB 2; Length 176;

Best Local Similarity 79.9%; Pred. No. 2.1e-50;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY 7 SLVSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCAG 66

Db 5 SHVSSLSHWF-----LLLLLLLLLPLVIFAMPESYSFNCPDGEYQSDNDVCKTCPSG 56

QY 67 TFVKAPCEIPHTQGCCKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATSDRKQC 126

Db 57 TFVKAPCKIPHTQGCCKCHPGTFTKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPESCRCCTKCPQIPVLQECNSTANTVCSSVS 170

Db 117 QIGLYYYDDPKFPESCRCCTKCPQIPVLQECNSTANTVCSSVS 160

RESULT 11

ADF57551

ID ADF57551 standard; protein; 176 AA.

XX AC ADF57551;

XX DT 12-FEB-2004 (first entry)

XX DE Mouse ymkz5 receptor.

XX KW Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour;

XX KW cancer; acquired immune deficiency syndrome; AIDS; anaemia;

XX KW autoimmune disease; cachexia; leprosy; leukaemia; hepatitis;

XX KW multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;

XX KW receptor.

XX OS Mus musculus.

XX PN US2003096355-A1.

XX PD 22-MAY-2003.

XX PF 11-JUL-2002; 2002US-00193616.

XX PR 09-JUL-1999; 99US-0143137P.

XX PR 07-JUL-2000; 2000US-00611989.

XX PA (ZHAN/) ZHANG K.

XX PI Zhang K;

XX WPI; 2004-008943/01.

XX DR N-PSDB; ADF57550.

XX Novel ymkz5-receptor polypeptide useful for treating diseases such as

XX tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy,

XX leukemia, hepatitis, multiple sclerosis.

XX Claim 13; SEQ ID NO 8; 57pp; English.

XX The invention relates to transmembrane decoy receptor, ymkz5 belonging to

XX tumour necrosis factor (TNF) receptor supergene family and nucleic acid

XX sequences encoding such receptors. The invention is useful for detecting

XX diseases or susceptibility to diseases related to the presence of mutated

XX ymkz5-receptor gene such as tumours or cancers. The sequences of the

XX invention are used as medication for a number of diseases such as

XX acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases,

XX cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial

XX ischaemia, obesity etc. The invention is also useful in gene therapy. The

XX present sequence is mouse ymkz5 receptor protein.

XX Sequence 176 AA;

Query Match

69.9%; Score 705; DB 8; Length 176;


```
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX W0200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS73531.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 39703; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (I). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 380 AA;
XX
XX Query Match 53.8%; Score 542.5; DB 4; Length 380;
XX Best Local Similarity 80.2%; Pred. No. 1.2e-36;
XX Matches 101; Conservative 0; Mismatches 0; Indels 25; Gaps 1;
XX
XX 8 LVSSLRWFLWRRLLLLLLLLLLLLLLLLPLQ-----VKFAMLE 42
XX
XX 47 LVSSLRWFLWRRLLLLLLLLLLLLLLLLPLQKAVHKATPESAIADCSGRDCAPVKVFAMLE 106
XX
XX 43 LHSFKPAGEYWSKDVCKKNCAGTFVKAPCEIPHTQOQCEKCHPGFTTEKDNVLDACIL 102
XX
XX 107 LHSFKPAGEYWSKDVCKKNCAGTFVKAPCEIPHTQOQCEKCHPGFTTEKDNVLDACIL 166
XX
XX 103 CSTCDK 108
XX
XX 167 CSTCDK 172
XX
XX RESULT 15
XX ADF57549
XX ID ADF57549 standard; protein; 117 AA.
```

```
XX ADF57549;
XX
XX 12-FEB-2004 (first entry)
XX
XX Mouse ymkz5 receptor from clone ymkz5-00013-g11.
XX
XX Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour;
KW cancer; acquired immune deficiency syndrome; AIDS; anaemia;
KW autoimmune disease; cachexia; leprosy; leukaemia; hepatitis;
KW multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
KW receptor.
XX
XX Mus musculus.
XX
XX US2003096355-A1.
XX
XX 22-MAY-2003.
XX
XX 11-JUL-2002; 2002US-00193616.
XX
XX 09-JUL-1999; 99US-0143137P.
XX
XX 07-JUL-2000; 2000US-00611989.
XX
XX (ZHAN/) ZHANG K.
XX
XX Zhang K;
XX
XX WPI; 2004-008943/01.
XX
XX N-PSDB; ADF57563.
XX
XX Novel ymkz5-receptor polypeptide useful for treating diseases such as
PT tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy,
PT leukemia, hepatitis, multiple sclerosis.
XX
XX Example 1; SEQ ID NO 6; 57pp; English.
XX
XX The invention relates to transmembrane decoy receptor, ymkz5 belonging to
CC tumour necrosis factor (TNF) receptor supergene family and nucleic acid
CC sequences encoding such receptors. The invention is useful for detecting
CC diseases or susceptibility to diseases related to the presence of mutated
CC ymkz5-receptor gene such as tumours or cancers. The sequences of the
CC invention are used as medication for a number of diseases such as
CC acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases,
CC cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial
CC ischaemia, obesity etc. The invention is also useful in gene therapy. The
CC present sequence is mouse ymkz5 receptor protein.
XX
XX Sequence 117 AA;
XX
XX Query Match 46.3%; Score 467; DB 8; Length 117;
XX Best Local Similarity 73.6%; Pred. No. 6.1e-31;
XX Matches 89; Conservative 5; Mismatches 19; Indels 8; Gaps 1;
XX
XX 7 SLVSSLRWFLWRRLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKPAGEYWSKDVCKKNCAG 66
XX
XX 5 SHVSSLRWFLWRRLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKPAGEYWSKDVCKKNCAG 56
XX
XX 67 TFVKAPCEIPHTQOQCEKCHPGFTTEKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
XX
XX 57 TFVKAPCEIPHTQOQCEKCHPGFTTEKDNVLDACILCSTCDKQEMVADCSATSDRKCEC 116
XX
XX 127 R 127
XX
XX 117 Q 117
XX
XX Search completed: September 9, 2005, 08:53:50
XX Job time : 545.286 secs
```